The External Quality Assurance System of the WHO Global Foodborne Infections Network, 2011

Hendriksen, Rene S.; Karlsmose, Susanne; Jensen, Arne Bent; Aarestrup, Frank Møller

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CDC
Centers for Disease Control and Prevention

international network Institut Pasteur

DTU Food
National Food Institute

THE EXTERNAL QUALITY ASSURANCE SYSTEM OF THE WHO GLOBAL FOODBORNE INFECTIONS NETWORK YEAR 2011

Rene S. Hendriksen, Susanne Karlsmose, Arne Bent Jensen, Frank M. Aarestrup

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www.food.dtu.dk

National Food Institute

Technical University of Denmark

Kemitorvet

Building 204

DK-2800 Kgs. Lyngby

Denmark

Tel: +45 35 88 70 00

Fax +45 35 88 70 01

Contents

List of Abbreviations

AMP, Ampicillin

AST, Antimicrobial Susceptibility Testing

ATCC, American Type Culture Collection

CAZ, Ceftazidime

CCM, Czech Collection of Micro-organisms

CHL, Chloramphenicol

CIP, Ciprofloxacin

CDB, Country Data Bank

CDC, Centers for Disease Control and Prevention

CLSI, Clinical and Laboratory Standards Institute

CRO, Ceftriaxone

CTX, Cefotaxime

DTU Food, Technical University of Denmark - National Food Institute

ESBL, Extended Spectrum Beta-Lactamase

EQAS, External Quality Assurance System

ERY, Erythromycin

EUCAST, European Committee on Antimicrobial Susceptibility Testing

GEN, Gentamicin

IATA, International Air Transport Association

IP. Institute Pasteur

MIC, Minimum Inhibitory Concentration

NAL, Nalidixic Acid

NSSC, National *Salmonella* and *Shigella* Center, Thailand

PHAC, Public Health Agency of Canada

QC, Quality Control

SMX, Sulfamethoxazole

STR, Streptomycin

SXT, Trimethoprim + Sulphonamides

TET, Tetracycline

TMP, Trimethoprim

WHO, World Health Organization

WHO GFN, WHO Global Foodborne Infections Network

1. Introduction

Since 2000, ten External Quality Assurance System (EQAS) reports have been issued with this report being the 11th. The WHO Global Foodborne Infections Network (WHO GFN)", focuses on enhancing World Health Organisation (WHO) Member States' capacity to detect and respond to foodborne disease outbreaks by conducting laboratory-based surveillance of *Salmonella* and other foodborne pathogens. Since its inception, the scope of WHO GFN has expanded to include additional foodborne pathogens like *Shigella* and *Campylobacter*. *Salmonella*, *Campylobacter* and *Shigella* are among the most important foodborne pathogens worldwide and account for millions of cases of diarrheal disease and thousands of deaths per year, impacting both developing and industrialized countries. Furthermore, the increased number of *Salmonella* and *Shigella* isolates which are resistant to antimicrobials is of major concern since these isolates are associated with infections characterized by increased morbidity and mortality.

The EQAS is organized annually by the National Food Institute (DTU Food), Kgs. Lyngby, Denmark in collaboration with Centers for Disease Control and Prevention (CDC) in Atlanta, USA; World Health Organization (WHO) in Geneva, Switzerland; Public Health Agency of Canada (PHAC) in Canada; National *Salmonella* and *Shigella* Center (NSSC), National Institute of Health, Department of Medical Sciences in Thailand and Institute Pasteur (IP) in Paris, France. The technical advisory group for the WHO EQAS program consists of members of the WHO GFN Steering Committee.

Individual laboratory data are confidential and only known by the participating laboratory, the EQAS Organizer (DTU Food) and possibly the respective WHO GFN regional centre. All summary conclusions are made public. The goal set by WHO GFN aim towards having all national reference laboratories perform *Salmonella* serotyping with a maximum of one deviation out of eight strains tested (error rate of 13%) and antimicrobial susceptibility testing (AST) with a maximum error rate of 10% (either <5% very major / major errors and <5% minor errors, or <10% minor errors, as defined further in this report).

2. Materials and Methods

2.1 Participants

A pre-notification announcement of the EQAS 2011 was made through the WHO GFN list server on April 22nd, 2011 and a reminder was sent on May 15th, 2011 (App. 1). The pre-notification was available in English, Spanish, Portuguese, French, Chinese and Russian, and included invitations to participate in the EQAS 2011 program for serotyping and AST of *Salmonella* and *Shigella*, identification and AST [Minimum Inhibitory Concentration (MIC) determination] of *Campylobacter*, and identification of an unknown foodborne pathogen. Participation was free of charge, but each laboratory was expected to cover expenses associated with the analyses performed.

2.2 Strains

Eight *Salmonella* strains, four *Shigella* strains, and two *Campylobacter* strains were selected for the EQAS 2011 from the DTU Food's strain collection. The unknown foodborne pathogen, an *Aeromonas hydrophila* strain, was selected by the Laboratory Subcommittee under the WHO GFN Steering Committee, and it was provided by PHAC, Canada. Individual sets of *Salmonella*, *Shigella*, and the unknown strain for identification were inoculated as agar stab cultures in nutrient agar. The *Campylobacter* strains were lyophilized in glass vials by Czech Collection of Micro-organisms (CCM), Czech Republic. The serotype of each *Salmonella* strain was determined based

on the O (somatic), phase 1 and phase 2 H (flagellar) antigens according to the scheme of Kaufmann-White (2007) [1]. The *Salmonella* serotypes were determined by DTU Food and verified by the CDC and IP prior to distribution. The antimicrobial susceptibility patterns of the *Salmonella*, *Shigella* and *Campylobacter* strains were determined by DTU Food and verified by CDC. The *Shigella* serotypes were performed by PHAC and verified by the NCCS. A final confirmation after production of agar sticks was performed at DTU Food (apart from *Shigella* serotyping which is not routinely performed at DTU Food).

Laboratories which did not formerly participate in the WHO GFN EQAS AST component were provided with lyophilized international reference strains, namely *E. coli* CCM 3954 ~ ATCC 25922 and *C. jejuni* CCM 6214 ~ ATCC 33560, purchased from the Czech Collection of Micro-organisms (CCM); The Czech Republic.

2.3 Antimicrobials

AST of the *Salmonella, Shigella,* and *Campylobacter* strains was performed at the DTU Food, and the obtained results were used as a reference standard (App. 2). The following antimicrobials were used for AST of *Salmonella* and *Shigella* strains: ampicillin, AMP; cefotaxime, CTX; ceftazidime, CAZ; ceftriaxone, CRO; chloramphenicol, CHL; ciprofloxacin, CIP; gentamicin, GEN; nalidixic acid, NAL; streptomycin, STR; sulfamethoxazole, SMX; tetracycline, TET; trimethoprim, TMP and trimethoprim + sulphonamides, SXT. In addition, it was possible to confirm the presence of Extended Spectrum Beta-Lactamase (ESBL)-producing strains by using the antimicrobials CTX and CAZ in combination with the inhibitor clavulanic acid. The following antimicrobials were used for AST of *Campylobacter* strains: chloramphenicol, CHL; ciprofloxacin, CIP; erythromycin, ERY; gentamicin, GEN; nalidixic acid, NAL; and tetracycline, TET.

MIC determination was performed by using Sensititre systems from Trek diagnostics Ltd, and guidelines and breakpoints by Clinical and Laboratory Standards Institute (CLSI) based on document M07-A8 (2009) “Methods for Dilution Antimicrobial Susceptibility Tests for Bacteria That Grow Aerobically”; Approved Standard - Eighth Edition [2], M100-S21 (2011) “Performance Standards for Antimicrobial Susceptibility Testing”; Twenty-First Informational Supplement [3], document M31-A3 (2008) “Performance Standards for Antimicrobial Disk and Dilution Susceptibility Tests for Bacterial Isolated from Animals”; Approved Standard - Third Edition [4], and document M45-A2 (2010) “Methods for Antimicrobial Dilution and Disk Susceptibility Testing of Infrequently Isolated or Fastidious Bacteria”; Approved Guideline – Second Edition [5]. Guideline were used for interpretation of AST results with the exception of i) ciprofloxacin susceptibility testing for which the EUCAST (European Committee on Antimicrobial Susceptibility Testing; www.eucast.org) epidemiological cut-off value was utilized; ii) streptomycin susceptibility testing for which DTU Food interpretative criteria was utilized; and iii) *Campylobacter* AST, for which EUCAST epidemiological cut-off values were used. For cefotaxime, ceftazidime and ceftriaxone values listed in CLSI M100-S21, supplemental Table 2A-S1 were utilized. All breakpoints are listed in the protocol (App. 3).

2.4 Distribution

Bacterial cultures were enclosed in double pack containers (class UN 6.2) and sent to participating laboratories according to the International Air Transport Association (IATA) regulations as “Biological Substance category B” classified UN3373. Prior to shipping, laboratories were informed about the dispatch date. Import permits were necessary for shipping the parcels to a number of countries. Many of the parcels were shipped as “overpack” through international hubs which offered to support the costs of further distributing the parcels. Helen Tabor from PHAC;

Canada, Matt Mikoleit from CDC; United States, Chaiwat Pulsrikarn from NSSC; Thailand, Francois Xavier Weill from IP; France, Rita Tolli from Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana, Italy and Rama Murthy from National Institute of Cholera and Enteric Diseases, India shipped to all Canadian, American, Thai, Francophone African, Italian and Indian institutes, respectively. From China, agreements were in place to send an overpack to Kan Biao from Institute for Communicable Disease Prevention and Control, Beijing, however, an import permit was not obtained why the Chinese overpack could not be dispatched. Most parcels were dispatched in August 2011, and the last in December, 2011.

2.5 Procedure

Participants were instructed to download the protocol (App. 3) and additional documents (App. 4a and 4b; available only in English) from http://www.antimicrobialresistance.dk/. In addition, they were requested to subculture the strains prior to performing the method routinely used in their laboratory. The EQAS components included serotyping and AST of eight *Salmonella* and four *Shigella* strains, identification and MIC determination of two *Campylobacter* strains, AST of two quality control (QC) strains (*E. coli* CCM3954 / ATCC25922, *C. jejuni* CCM 6214 / ATCC33560), and identification of an unknown foodborne pathogen (*Aeromonas hydrophila*). Furthermore, the laboratories were requested to save and maintain the ATCC reference strains for future proficiency tests (App. 4a and 4b).

After performing the tests, participants were requested to submit i) the obtained results (serogroup and / or serotype, MIC values or zone-diameter in millimeters, and antimicrobial susceptibility categories of the *Salmonella* and *Shigella* strains; ii) identification, MIC values, and antimicrobial susceptibility categories of the *Campylobacter* strains; iii) identification of the unknown strain). The results were to be submitted to an electronic record sheet in the WHO GFN web-based database through a secured individual login, or alternatively, to send the record sheets from the enclosed protocol by fax to DTU Food. The database was activated on September 2nd, 2011 and closed on March, 14th, 2012.

The *Salmonella* and *Shigella* strains were categorized as resistant (R), intermediate (I) or susceptible (S) to all tested antimicrobials, whereas the *Campylobacter* strains were categorized as resistant (R) or susceptible (S) to all tested antimicrobials. The interpretative criteria followed to generate the results used as reference standard were based on both clinical breakpoints and epidemiological cut-off values as described above.

Of note, the authors would like to state that the terms ‘susceptible’, ‘intermediate’ and ‘resistant’ should be reserved for classifications made in relation to the therapeutic application of antimicrobial agents. When reporting data based on epidemiological cut-off values, bacteria should instead be reported as ‘wild-type’ or ‘non-wild-type’ [6]. Due to the different AST methods used by the participants and to simplify interpretation of the results, throughout this report we will maintain the terms susceptible, intermediate and resistant also when we refer to wild-type and non-wild-type strains.

Susceptibility results had to be interpreted on an individual basis for each antimicrobial tested according to the values listed in the protocol (App. 3). Participants were instructed to use the *Salmonella / Shigella* antisera and the antimicrobials used in the methods routinely performed. In addition, they were instructed to submit the breakpoints routinely applied in their laboratory for categorizing AST results, if different from those listed in the protocol. All laboratories were requested to enter MIC values for the *C. jejuni* (ATCC 33560) reference strain, and either zone diameters or MIC values for the *E. coli* (ATCC 25922) reference strain. After submitting the results,

participants were instructed to retrieve an instantly generated report from the secure web site. This report was created on an individual basis, and reported all deviations from the expected results and suggestions for solving or investigating the cause of error. Deviations of antimicrobial susceptibility test results from the expected results were categorized as minor, major or very major. Minor deviations are defined as classification of an intermediate strain as susceptible, resistant or vice versa (*i.e.* I ↔ S or I ↔R). Major deviation is the classification of a susceptible strain as resistant (*i.e.* S → R). Very major deviation is the classification of a resistant strain as susceptible (*i.e.* R → S). In this report, the deviations of AST results are divided into two categories, *i.e.* critical deviations which include major and very major deviations, and total deviations which include also the minor deviations.

3. Results

A total of 183 laboratories responded to the pre-notification and were enrolled in the EQAS. When the deadline for submitting results was reached, 166 laboratories in 90 countries had uploaded data. The following countries provided data for at least one of the EQAS components (Figure 1): Albania, Argentina, Australia, Barbados, Belarus, Belgium, Bolivia, Bosnia and Herzegovina, Brazil, Brunei Darussalam, Bulgaria, Cambodia, Cameroon, Canada, Central African Republic, Chile, Colombia, Democratic Republic of Congo, Costa Rica, Croatia, Cuba, Cyprus, Czech Republic, Denmark, Ecuador, Egypt, Estonia, Ethiopia, Finland, France, Gabon, Georgia, Germany, Ghana, Greece, Grenada, Guatemala, Honduras, Hungary, India, Iran, Ireland, Israel, Italy, Ivory Coast, Jamaica, Japan, Jordan, Kenya, Korea, Lao, Lithuania, Luxembourg, Madagascar, Malaysia, Malta, Mauritius, Mexico, Morocco, Nepal, New Zealand, Nicaragua, Nigeria, Sultanate of Oman, Palestine, Panama, Paraguay, Peru, Philippines, Poland, Russia, Serbia, Seychelles, Singapore, Slovakia, Slovenia, South Africa, Sri Lanka, Sudan, Suriname, Taiwan, Thailand, Tunisia, Turkey, United Kingdom, Uruguay, USA, Venezuela, Vietnam, Zambia. It's noteworthy to mention that due to import permit issues, China did not participate in the EQAS 2011; therefore the following part of the report does not refer to the strains intended for the 12 registered Chinese participants.

In the description of results, arbitrary thresholds of quality limits were not used. The results for AST are expressed as correct, minor, major, very major, and critical and total deviations as described above.

3.1 Methods used by EQAS participants

A total of 167 laboratories received *Salmonella* strains, and 144 (86%) participated in the *Salmonella* serogrouping component of the EQAS, whereas 123 (74 %) participated in the complete serotype module of the EQAS. In addition, 127 (76 %) laboratories submitted AST results. Among the laboratories performing AST, 111 (87 %) submitted results for the quality control (QC) strain *E. coli* ATCC 25922. The majority (n=88; 79 %) of these laboratories used the disk diffusion method, while a MIC determination method was utilized by a smaller number (n=23; 21 %) of laboratories.

Of 131 laboratories receiving *Shigella* strains, 109 (83 %) submitted *Shigella* serogroup results (speciation) and 66 (50 %) of these laboratories serogrouping the isolates further analyzed the strains to the serotype level. In addition, *Shigella* AST was performed by 107 (82 %) of these laboratories.

All participating laboratories were through the protocol given information regarding the breakpoints used for interpretation when generating the expected interpretation. Expected values were given as MIC-values only. In addition, all participating laboratories were instructed on interpretation of resistance to third generation cephalosporins and to fluoroquinolones.

Of the 123 laboratories receiving *Campylobacter* strains, 81 (66 %) reported identification results and 32 (26 %) submitted AST results for both *Campylobacter* strains.

Of the 138 laboratories receiving the unknown culture for identification, 106 (77 %) submitted results.

3.2 Serogrouping and serotyping of *Salmonella* strains

In 2011, the percentage of laboratories reporting complete serotype results for all eight strains increased to 89% (n=109), thus continuation of the increasing trend observed since 2008. However, the number of participants submitting results for all eight isolates did not follow the same trend as it decreased by 20 participants from 2010 to 2011. The proportion of correctly serotyped strains increased from 89% (n=998) in 2010 to 92% (n=878) in 2011 but faced the same issue with a lower number of participants submitting data (Table 1).

In Table 2, the number of participating laboratories is reported according to the number of correctly serotyped samples. In 2011, 82 (67%) of the 123 participating laboratories serotyped all eight strains correctly, and 17 (14%) laboratories correctly serotyped seven of the eight strains. In summary, in 2011, a total of 99 (81%) participating laboratories met the threshold for adequate performance of *Salmonella* serotyping, which represents a considerable increase compared to 2010 where 107 (72%) of the participating laboratories met the performance quality threshold. In addition, 91% of the participating laboratories correctly identified half of the strains, which represents a 5% increase compared to 2010 (86%). Furthermore in 2011, all participants had at least one isolate correctly serotyped which was last observed four years ago.

In Table 3, the performance of *Salmonella* serotyping is reported on a region-based categorization of participating laboratories. Overall, the accuracy of serotyping again this year increased in most regions compared to 2010. One region, Latin America, experienced an influx of EQAS participants in 2011. The other regions experienced either a slight decrease from one to three participants in 2011 or had a constant level of participants. In 2011, the Chinese region could unfortunately not participate due to import permit issues.

The number of tested strains decreased in most in regions with exception in Central Asia & Middle East, Latin America, and Southeast Asia. The accuracy of serotyping was constant or increased in most in laboratories compared to 2010. The most profound increases were observed in Africa, Central Asia & Middle East, and Southeast Asia. A decrease in accuracy of serotyping was only observed in Caribbean and North America compared with 2010.

The overall performance of laboratories performing *Salmonella* serogrouping was excellent compared to 2010 with seven of the isolates having af deviation level below 5% and ranging from 0.7% (WHO S11.4; Derby) to 5.8% (WHO S11.2; Westhampton) (Table 4).

Of 130 laboratories performing serotyping of the internal quality control strain (WHO S11.7, used in EQAS 2000, 2001, 2004, 2006, 2007, 2008, 2009, and 2010), 128 (98%) reported a correct result, thus leading to a deviation rate of only 2% (Table 4). Thus in 2011, the ability of participating laboratories to correctly serotype the internal quality control strain was again the highest ever recorded from the beginning of the WHO EQAS (Table 5). A deviation of only 2% (to be precise, 1.5%) is an outstanding result.

Deviations in *Salmonella* serotyping ranged from 1.5% (WHO S11.7) to 14.4% (WHO S11.4) (Table 4). In 2011, all but one of the isolates (WHO S11.4 Derby, 14.4%; WHO S11.8 Berta 10.1%) exhibited deviation levels above the magic number of 10% (Table 4).

3.3 Antimicrobial susceptibility testing (AST) of *Salmonella* strains

A total of 11,353 antimicrobial susceptibility tests were performed in 2011 by 127 participating laboratories (Table 8). Of the submitted results, 91% were in agreement with the expected result, which is a slight reduction compared to 2010 – the second year in a row where a decrease have been observed (Table 6). Minor, major and very major deviations were observed in 4%, 2% and 3% of the submitted results, respectively (Table 6).

Some difficulties in assessing antimicrobial susceptibility were encountered for the tested combinations of strains and antimicrobials. The difficulties were mainly in assessing susceptibility to the usual antimicrobial suspects; STR and CIP, and especially showed for the isolates WHO S11.4 Derby and WHO S11.6 Onireke (Table 7).

Major deviations categorized by tested antimicrobial are reported in Table 8. Notably, a large number of critical deviations were observed for CIP (20%). This antimicrobial together with STR, NAL, and TET also resulted in very high numbers of total deviations (Table 8). In 2011, we maintained the average number of overall critical and total deviations with 5% and 9%, respectively.

In 2011, the number of laboratories participating in the AST component of EQAS decreased in all regions with exception of Southeast Asia (Table 9). Unfortunately, the largest decrease were observed in regions consisting mainly of developing countries needing guidance, such as in Africa, decreasing with five laboratories (23% reduction compared to 2010), Central Asia & Middle East decreasing with three laboratories (42% reduction compared to 2010), and Caribbean decreasing with two laboratories (50% reduction compared to 2010). Overall, the performance of AST differed in all regions, most notably in the African and Caribbean regions where the performance (percent correctly tested) increased from 84.7% in 2010 to 87.0% in Africa and from 90.9% in 2010 to 96.5% in 2011. Overall, 87.0% (Africa) of the antimicrobial susceptibility test results to 96.5% (Caribbean) were reported correctly (Table 9).

Antimicrobial susceptibility to *E. coli* ATCC 25922 was tested by 23 laboratories with the MIC determination method and by 88 laboratories with the disk diffusion method. The proportion of laboratories which submitted values outside the acceptable interval for the reference strain *E. coli* ATCC 25922 is reported in Table 10. The percentages of laboratories which reported MIC values outside the intervals accepted for the QC strain ranged from 0% (CHL, CTX, NAL, and TMP) to 9% (CIP and GEN) (Table 10). These results indicate that there is no consistency with what caused problems in 2011. In general, laboratories using the MIC determination method reported values within the acceptable interval in higher percentages compared to the laboratories using the disk diffusion method, with the exception to CAZ, CIP, and STR testing (Table 10).

3.4 Serogrouping and serotyping of *Shigella* strains

Like in 2010, the performance of *Shigella* speciation was highly satisfactory in 2011, as the percentages of deviations were very low for all the four test strains, ranging from 0.9% (WHO SH 11.4) to 2.8% (WHO SH 11.1 and WHO SH 11.2) (Table 11). The deviations observed among laboratories performing full serotyping were satifactory ranging from 5.7 % (WHO SH 11.1) to 11.7% (WHO SH 11.4). The strain resulting in most deviations was WHO SH 11.4: *Shigella flexneri* serotype 1b, reported as serotype 1a and 3a by six and one participating laboratories, respectively.

In Table 12, the performance of *Shigella* serotyping is reported according to geographical distribution of participating laboratories. The majority of participating laboratories was located in Latin America (n=15), Southeast Asia (n=13), and Europe (n=16). The number of participating

laboratory decreased in most regions compared to 2010 with exception of Europe and Latin America. The accuracy of *Shigella* serotyping results were in many regions excellent ranging from 84.8% (Southeast Asia) to 100% (Africa, Central Asia and Middle East, Oceanic, and North America). Unfortunately, the Caribbean countries did not participate in the *Shigella* component.

3.5 Antimicrobial susceptibility testing (AST) of *Shigella* strains

A total of 4,184 antimicrobial susceptibility tests were performed in 2011 by 107 participating laboratories. Agreement with the expected result was achieved in 92% of the reported results, which is still a reduction compared to 2009 (Table 13). Minor, major and very major deviations were observed in 2%, 1% and 4% of reported results, respectively (Table 13).

Difficulties in assessing antimicrobial susceptibility to CIP and CAZ was encountered as resistance in isolate WHO SH-11.4 (Table 14). CAZ, CIP, NAL, and STR accounted for 12.0%, 40.7%, 11.0% and 10.5% of total deviations, respectively (Table 15).

Two ESBL-producing *Shigella* strains were included in the EQAS 2011 trial. The participating laboratories had between 2.0% and 12.0% deviating results for CAZ, CRO, and CTX (Table 15).

In 2011, all participating regions partook in the *Shigella* AST component. The majority of participating laboratories was located in the European, Latin American, Southeast Asian and African regions where 24, 20, 19 and 16 laboratories participated to this EQAS iteration, respectively (Table 16). By considering participating laboratories in relation to their geographical location, the percentage of correct AST results ranged from 86.0% (Africa) to 97.7% (Caribbean). The African, North American, and Southeast Asian regions reported results presenting the highest percentages of critical and total deviations, *i.e.* 11.9%, 9.2%, and 6.9% critical deviations, and 13.7%, 9.2%, and 9.0% total deviations, respectively (Table 16).

3.6 ESBL-producing *Salmonella* and *Shigella*

An optional part of the EQAS was to detect and confirm Extended-Spectrum Beta-Lactamase (ESBL) production. If participating in this item of the EQAS, all strains showing reduced susceptibility to cefotaxime (CTX), ceftazidime (CAZ) and/or ceftriaxone (CRO) should be tested for ESBL production.

One of the *Salmonella* (WHO S-11.5), and two of the *Shigella* (WHO SH-11.2 and WHO SH-11.4) test strains were ESBL-producing. The WHO S-11.5 (*Salmonella* Havana) harboured the $bla_{\text{CTX-M-15}}$ gene whereas WHO SH-11.2 *Shigella sonnei* and WHO SH-11.4 *Shigella flexneri* serotype 1b harboured the $bla_{\text{CMY-2}}$ and $bla_{\text{CTX-M-15}}$ gene, respectively. Uploaded results regarding ESBL-producing strains are listed in Table 17 presenting the fact that up to 8% of the uploaded results for the confirmatory testing were deviating.

3.7 Identification of *Campylobacter* strains

Participation in the EQAS 2011 *Campylobacter* component was requested by 122 laboratories (disregarding China), of which 81 (66%) submitted results within the deadline. Of the participating laboratories, 59% and 70% performed correct species identification for strain #1 (*C. coli*) and #2 (*C. coli*), respectively (Table 18). A considerable large number of laboratories; 19 and 17 reported #1 and #2 being *C. jejuni.*

In Table 19, the performance of *Campylobacter* identification is reported according to geographical location of participating laboratories. The majority (n=25; 31%) of participating laboratories were as in 2009 and 2010 located in Europe, but a large number of participates were also observed Latin

America (n = 19). The accuracy in *Campylobacter* identification ranged from 0% (Caribbean) to 100% (Oceanic region). In 2011, the performance dropped tremendously compared to 2010 in regions with exception of Oceania.

3.8 MIC determination of *Campylobacter* strains

A total of 387 MIC determinations were performed in 2011 by 32 participating laboratories (Table 22). Among the reported results 93.8% were in agreement with the expected result (Table 20). Major and very major deviations were observed in 2.8% and 3.4% of reported results (Table 20).

WHO C-11.2 created a few difficulties in assessing antimicrobial susceptibility for STR and TET (Table 21). This was likewise displayed in the overall performance by antimicrobial where 13.3% and 8.3% deviations were reported for STR and TET, respectively (Table 22).

In 2011, MIC values were submitted by almost all laboratories with exception of Caribbean (Table 23). An increase in participation was observed in Africa going from two laboratories to six. Agreement with expected values was observed in percentages ranging from 75.0% (Central Asia and Middle East) to 100% (Europe, North America, Oceania, and Russia) (Table 23). The highest percentages of critical deviations were reported from laboratories in Africa, Central Asia and Middle East, and Southeast Asian regions 17.3%, 25.0, and 15.0%, respectively (Table 23).

MIC values of reference strain *C. jejuni* ATCC 33560 were tested by 26 laboratories. Of these, 17 laboratories used micro-dilution procedures, while nine laboratories used agar-dilution procedures and tested only CIP, ERY and GEN. Overall, the percentage of laboratories which submitted values within the acceptable interval for the reference strain seemed to experience most problems with CIP and ERY, which showed 77% and 75% results within range, respectively. (Table 24).

3.9 Identification of the unknown culture

Identification of the unknown enteric pathogen (*Aeromonas hydrophila*) was performed by 106 laboratories (Table 25). Overall, 83% of the participating laboratories identified the strain as *Aeromonas hydrophila*.

4. Discussion

4.1 Serogrouping and serotyping of *Salmonella* strains

As in previous years, the selection of serovars included in the 2011 WHO GFN EQAS trial was based both on the 15 most common serovars submitted to the WHO GFN Country Data Bank (CDB) [7] and on various reports and scientific publications. To facilitate the global assessment of *Salmonella* serotyping capacity, we chose serovars which may be very common in certain regions and sporadically encountered in other regions. In 2011, we included *Salmonella* Enteritidis as in previous years as it serves as internal control but also as it is one of the most frequent serovars worldwide despite a decreasing trend. *Salmonella* Derby; a pig related serovar seems to be quite frequent in Europe ranking high on the top 20 list whereas it appears to be less frequent in Southeast Asia and South Americas, however, still among top 20. In the other regions, *Salmonella* Derby is not listed among top 20 causing human illness [7]. Another relatively frequent serovar; *Salmonella* Muenchen was included the EQAS 2011. This serovar is moderately common in North America and South America and ranked low in the top 20 in Europe. In 2011 EQAS, a number of less common to rare serovars were included such as *Salmonella* Abaetetuba and *Salmonella* Onireke. *Salmonella* Abaetetuba has been described causing infections in sea lizards from the Galapagos Islands [8] whereas *Salmonella* Onireke has been isolated from chicken from Nigeria. It has been

speculated that this serovar might originate from the environment and reptiles [9]. *Salmonella* Haifa has been reported in several cases associated with poultry in Africa e.g. Ethiopia and Nigeria [9] but also causing diarrhea in humans including travelers. The serovar also seems to be a rare encounter. Another poultry related serovar; *Salmonella* Havana was included the panel of EQAS isolates. This serovar seems not to be frequent but there is evidence of it being found in multiple reservoirs including camels, pigs, raptors, birds, and including infection in humans [10]. Lastly, *Salmonella* Westhampton was included the EQAS panel. This serovar is as most of this year's panel infrequently found around the world. Overall, the panel of 2011 was greatly influenced by rare or infrequently observed serovars hopefully making the participants curious of their nature.

The number of laboratories which serotyped all eight *Salmonella* strains increased once again to 89% (n = 109) in 2011, which represents the best results since 2000 where 92% of the participants tried to serotype all of the eight serovars. However in 2000, only 34 participants serotyped all eight isolates. We also observed a minor increase in performance compared to 2011. This might be due to the lower number of participants in this year's EQAS lacking the countries performing less well. This seems to be the case in all test in this year's EQAS. It is of course nice to see a positive increase in performance but at the same time unfortunate to observed that developing countries might ignore the EQAS invitation due to previous years' poor results. One of the purposes of the EQAS is also to identify areas where training is needed or resources are poor.

Similar to the result of participants attempting to serotype all isolates, the percentage of correctly serotyped strains also increased to the best result ever recorded. This also indicates the hypothesis indicated above. However, it is still an excellent achievement to have 92% (n=109) of the participants correctly serotype the eight *Salmonella* isolates.

The isolates included in this year's EQAS are not believed to be easier to type compared to the last couple of years as we in 2011 have four isolates containing the G complex which often is a challenge due to the many different antisera needed to pin out the correct antigens. Furthermore, two isolates were of a less common somatic antigen e.g. O:11 and O:13. Similarly, one isolate contained a z_{10} H-antigen – all contributing to a moderate level of difficulty.

An astonishing 98% of participating laboratories correctly serotyped the internal control strain this year, and thereby even exceeded the 97% from the 2010-iteration. This is again the highest percentage recorded since the beginning of the EQAS. The quality threshold of correctly serotyping at least seven strains was met by 81% of participating laboratories, thus demonstrating once again an excellent improvement compared to previous years.

In general, the obtained results indicate that most laboratories worldwide have the capacity to serotype the most common *Salmonella* serovars. It is noteworthy that many developing regions obtained better results compared to 2010 which is truly an impressive accomplishment. However, a small reduction of participants was also observed from specifically those regions lacking potentially poor performers.

In 2011, main problem in serotyping the isolates are the same as in previous years with exception of 2010. The problem is linked to difficulties in the characterization of flagellar antigens. In 2011, especially the Complex G played a significant role in the number of incorrect identification of the serotypes. This most likely is a consequence of a lack of good quality antisera, financial resources, and availability. However, we believe this problem will be diminished with time due to the advancing of new sequence-based molecular techniques and the decreasing price of those methods. In the future, we foresee that multi locus sequence typing (MLST) and whole genome sequencing will replace conventional microbiological techniques such as serotyping and identification of resistance genes, plasmids, virulence genes etc. [11, 12]

4.2 Antimicrobial susceptibility testing (AST) of *Salmonella* strains

Overall, 91% of the *Salmonella* AST was correctly performed, and critical deviations were 5%. This result is still satisfactory but is still a decrease in performance since 2009. Noteably, the number of participating laboratories in the antimicrobial susceptibility testing component has now decreased since in 2008 from 168 to 127 in 2011. This is a highly worrisome development as the level of antimicrobial resistance is increasing with a tendency of creating more multi drug resistance pathogens. We need to strengthen the awareness about antimicrobial resistance and the need for performing antimicrobial susceptibility testing accurately.

In 2011, we followed the guidelines for MIC breakpoint interpretation as well as the expert guidelines on the interpretation of cephalosporin resistance which was distributed in 2010. Similarly, participating laboratories were asked to utilize EUCAST epidemiologic cut off values for interpretation of CIP susceptibility. The EQAS organizers utilized the lower epidemiologic cut off value for ciprofloxacin to facilitate the detection of low-level resistance which may be caused either by alteration of the drug target due to a single point mutation in the gyrase-encoding gene or by protection of the drug target due to qnr proteins which are encoded by plasmid-mediated genes. Of note, low-level ciprofloxacin-resistant strains (extra-intestinal non-typhoid *Salmonella* and *S.* Typhi) would be interpreted as intermediate according to the newly issued CLSI clinical breakpoints. However, this will not determine plain non-typhoid *Salmonella* or extra-intestinal non-typhoid *Salmonella* and *S.* Typhi as resistant toward fluoroquinolones even by using the new CLSI guidelines of 2012 why we maintain the EUCAST guidelines for interpretation of these compounds.

As in previous years, a high percentage of total deviations was observed for CIP, STR, and TET susceptibility tests. Interestingly, SMX susceptibility tests seemed not to create that many deviations in 2011 compared to previous years. In contrast, CIP and NAL seemed to cause some challenges in 2011 which was linked to detection of *qnr* genes in isolate WHO S-11.4 and WHO S-11.6 where participants indicated those isolates incorrectly as intermediate or resistant for NAL and the opposite for CIP. In the case of STR susceptibility test, the difficulties in testing this compound appear to be continuous. In Europe, discussions have been raised about the value of keeping this drug in the panel of antimicrobials ideal for monitoring. Publications suggesting new and updated cut off values for STR have also shown an overlapping distribution between the wild-type and non-wild-type complicating the exact determination of the resistant population [13].

In the case of SMX susceptibility test, we observed a decrease in deviating results in 2011 compared to those of EQAS 2010. A pit fall as regards reading the result of this antimicrobial is caused by the fact that it is bacteriostatic meaning that the zone diameter or the MIC should be read at 80% reduction of growth. A common mistake for this antimicrobial is therefore to register false resistance. This year, four of the test strains were resistant to SMX compared to two in 2010 which might explain the decrease in deviating results.

In general, data from the *Salmonella* AST component of EQAS 2011 demonstrate a minor reduction in the performance compared to 2009 and 2010. Of note, laboratories in Africa and Caribbean performed better compared to 2010 whereas Central Asia and Middle East, North America, Russia, and Southeast Asia obtained less correct test results compared to 2010.

When performing AST, the inclusion of reference strains for internal QC is extremely important. If correctly used, the reference strain will provide QC for both the method and the reagents. Unfortunately, only 111 (87%) participating laboratories submitted AST results of the QC strain. Thus a better result compared to 2010. We always encourage laboratories to conduct quality assurance when performing AST. To facilitate the internal QC, we provide each new participating laboratory with the reference strain *E. coli* ATCC 25922. Laboratories participating in EQAS are

invited to retain and maintain the QC strain for future use. As a rule, results for the test organisms should not be reported if ≥ 3 out of 30 results for the QC strain are outside the expected interval. In 2011, we observed an improvement in AST of QC strains using MIC determination compared to 2010 where the range of participants reporting results outside of the QC range were between 10% to 36% for CHL, CTX, NAL, TMP in contrast to no deviations in 2011. Compared to disk diffusion, similar or worse results were obtained in 2011 as to data outside the QC ranges. These erroneous disk diffusion results typically arise from inadequate standardization of methodologies, lack of good quality culture media and improper storage of antimicrobial-containing disks. Thus, deviations in AST results can likely be corrected by improving QC practices.

4.3 Serogrouping and serotyping of *Shigella* strains

In EQAS 2011, 104 to 109 correctly identified the four *Shigella* isolates resulting in a deviation range of 0.9% to 2.8% showing a high capacity within *Shigella* diagnostics.

Only half (48%-66%) of the participants conducting correct identification carried on and performed the serotyping. For WHO SH-11.4 (*S. flexneri* serotype 1b) causing most deviations in serotyping, six participants failed to detect the right serotype among antigen 1.

Most regions encountered a drop in participation where only participation increased in Europe and Latin America. However, in several regions no serotyping errors was recorded e.g. Africa, Central Asia and Middle East, North America and Oceania indicating the same hypothesis as for the *Salmonella* component that the developing countries are lacking in 2011 which in previous years obtained poor results.

4.4 Antimicrobial susceptibility testing (AST) of *Shigella* strains

In EQAS 2011, AST of *Shigella* spp. was performed by 107 laboratories which is a slight increase compared to 2009 and 2010. A total of 92% of the participants obtained a correct AST results which is within the same level as for AST in *Salmonella*. In comparison with the *Salmonella* results, a few more deviations categorized as minor were observed in contrast to fewer major and very major deviations. Overall, the AST results of the *Shigella* component were equal to what was seen in 2010. One could speculate if some laboratories participate in either the *Shigella* or the *Salmonella* AST component as the reason why the level of participation appear to have been declining over the years.

The results show that especially isolate WHO SH-11.4 caused some problems susceptibility testing towards CAZ, CHL, CIP, and NAL. In general, a large proportion of deviations testing CIP and CAZ were observed associated with isolates WHO SH-11.2 and WHO SH-11.4 that also were ESBL producers.

Accordingly, we observed high percentages of deviations related to CAZ, CIP, NAL, and susceptibility test results. The reason why some laboratories obtain deviations when testing CAZ might be the weakness of the antimicrobial for testing e.g. bla_{CTX} genes and ampC's which both isolates harboured. The high number of deviations to CIP and NAL were the same as for *Salmonella*. Surprisingly, participating laboratories performed SMX and TET susceptibility testing of *Shigella* more correctly than in *Salmonella*. This has also been observed in other EQAS towards *E. coli* conducted in Europe. Apparently, *E. coli* and *Shigella* do not present the same challenges with those compounds as *Salmonella*.

All regions submitted results with an overall regional performance similar to the one described for *Salmonella* AST differing with a maximum of 5%.

4.5 ESBL-producing *Salmonella* and *Shigella*

An emerging problem worldwide is ESBL-producing gram-negative bacteria. Three test strains, one *Salmonella* (WHO S-11.5) and two *Shigella*, (WHO SH-11.2 and WHO SH-11.4) were ESBL-producers and therefore relevant for the component of the EQAS including detection and confirmation of this phenotype.

The WHO S-11.5 (*Salmonella* Havana), WHO SH-11.2 *Shigella sonnei* and WHO SH-11.4 *Shigella flexneri* serotype 1b harboured $bla_{\text{CTX-M-15}}$, $bla_{\text{CMY-2}}$ and $bla_{\text{CTX-M-15}}$ genes, respectively. Some of the genes, e.g. bla_{CTX} genes and ampC's may not confer resistance to all cephalosporins, for example, CAZ appears to be an antimicrobial that does not always detect ESBL-producers. In general, it is recommended that more than one cephalosporin is used for the detection of an ESBL-producing *Salmonella* when initially screening the isolate. The cephalosporins cefotaxime, cefpodoxime, ceftiofur, ceftriaxone, and ceftazidime were all found useful in detecting isolates with ESBL or plasmidic ampC by Aarestrup *et. al.* [14], however, cefotaxime, cefpodoxime, and ceftriaxone were superior to the other two.

4.6 Identification of *Campylobacter* strains

In 2011, we selected only *Campylobacter coli* strains. Interestingly, since 2003 where this component was implemented the WHO EQAS, we have never observed correct identification of *C. coli* exceeding 85% (2010). In contrast, correct identification of *Campylobacter jejuni* seems to be easier as both 92% and 95% of correct identification of *C. jejuni* were obtained in 2010 and 2009, respectively. One of the explanations may be that when conducting a conventional hippurate hydrolysis test, that some *C. coli* are incorrectly identified based on false positive hippurate hydrolysis test results. The weakness of the conventional hippurate hydrolysis test is that sometimes the test suspensions develop a weak bluish color when testing *C. coli* that for the untrained person often will be mistaken as being positive indicating *C. jejuni.* We noticed a huge difference in performance per region in the different years. The regions performing less satisfactory one year performed well the following year. However, this may be the result of the panel containing either *C. jejuni* or *C. coli.* Overall, the results related to *Campylobacter* identification were poor compared to 2010.

4.7 Antimicrobial susceptibility testing (AST) of *Campylobacter* strains

In EQAS 2011, 32 laboratories participated in the MIC determination and performed overall satisfactorily, since they obtained 93.8% correct test results. In contrast to 2010, only minor problems testing the antimicrobials were observed. WHO C-11.2 created some minor problems when mainly testing STR and TET resulting in 13.3% and 8.3% critical deviations. There is no obvious explanation to these deviations. In 2011, laboratories from the Central Asia & Middle East and the Oceanic regions participated in this EQAS component. In contrast, the Caribbean did not participate.

In 2011, 26 (81%) participating laboratories submitted AST results for the QC strain. The majority of deviations were observed for CIP and TET susceptibility testing by micro-dilution at 42 °C and GEN susceptibility testing by micro-dilution at 37 °C. Interestingly, we noticed the same deviations as for 2010. Some problems were observed towards testing ERY when agar dilution at 42 °C was used, and hardly any when agar dilution at 37 °C was used. In general, AST of the QC strain was satisfactory.

4.8 Identification of the unknown culture

In EQAS 2011, we included an *Aeromonas hydrophila* strain to see how effectively the participants can differentiate *Aeromonas* from *Vibrio spp.* Of 106 laboratories delivering results, 88 (83%) identified the strain correctly. Only five participants indicated the unknown isolate as being a *Vibrio spp.* This indicates that most laboratories in fact are able to distinguish between *Vibrio* and *Aeromonas*.

5. Conclusions

The acceptance threshold for the *Salmonella* serotyping EQAS component was met by 81% (n=99) of the participating laboratories. In addition, 89% of the laboratories tested all eight strains and a total of 92% of all tests were correct, thus representing an increase compared to 2010. Additionally, the ability in correctly testing the internal QC strain increased from 97% in 2010 to 98% this year.

This year, the obtained results indicate that most laboratories worldwide have the capacity to serotype the most common *Salmonella* serovars. It is noteworthy that many developing regions obtained better results compared to 2010 which is truly an impressive accomplishment. However, a small reduction of participants was also observed from specifically those regions lacking potentially poor performers.

The main problem as regards serotyping appears to have been linked to difficulties in the characterization of flagellar antigens. In 2011, this especially concerns the Complex G and is most likely a consequence of a lack of good quality antisera, financial resources, and availability. In the future, however, it is likely that sequence-based molecular techniques will be competitive with traditional typing methods.

Concerning the *Salmonella* AST component, it is important to stress the importance of harmonizing the methodology and having adequate guidelines available. The EQAS 2011 results as regards AST of *Salmonella* showed a slight decrease of performance. Overall, the acceptance threshold was met, and we identified 4% minor and 5% critical deviations. CIP, NAL, STR and TET caused the majority of the observed deviations. Compared to 2010, laboratories in Africa and Caribbean performed better, whereas Central Asia and Middle East, North America, Russia, and Southeast Asia obtained less correct test results.

Strengthened awareness of the importance of performing internal quality control is crucial and is introduced in many of the participating laboratories. Sixteen (13%) participating laboratories did not report data for AST of the QC strain, though, despite the EQAS organizers repeated recommendation of the use of such QC strains and the provision of certified strains to new participants. The component related to AST of the QC strain was in general less satisfactory than in previous years. It is important to emphasize that this component represents the true indicator of the quality of AST performance.

For the *Shigella* component in EQAS 2011, consisting of of serogrouping, serotyping and AST, most laboratories correctly serogrouped the four *Shigella* strains, and a maximum of 2.8% deviations was observed. A total of 65 laboratories performed serotyping. Only minor regional differences were observed, and the highest number of deviations was reported from laboratories from the South East Asian region.

The results obtained in the *Shigella* AST component suggest conclusions similar to the ones reported above concerning the *Salmonella* AST.

Detection and confirm Extended-Spectrum Beta-Lactamase (ESBL) production has been included as an optional part of this EQAS due to the emerging importance of the phenotype in gram-negative bacteria. One of the *Salmonella* (WHO S-11.5), and two of the *Shigella* (WHO SH-11.2 and WHO SH-11.4) test strains were ESBL-producing. The obtained results indicate that there is still room for improvement in this context.

A total of 123 laboratories received *Campylobacter* for identification, but only 81 laboratories uploaded data. Both strains were *C. coli* and the difficulties in identifying these (59% and 70% correct results for the two strains) might be caused by issues with the hippurate analysis. The majority of difficulties in *Campylobacter* identification were experienced by laboratories in the regions of Africa, Central Asia & Middle East, the Caribbean, Russia and Latin America.

EQAS 2011, a total of 32 laboratories participated in MIC determination of *Campylobacter*. The acceptance threshold used for *Salmonella* was applied and was almost met, since we observed 6.2% critical deviations overall, and the data on antimicrobial level revealed that NAL, STR and TET susceptibility testing were the most challenging. Of the 32 participating laboratories, 26 performed AST of the QC strain. For this strain, the highest level of results outside the QC-range were seen for CIP and ERY.

The unknown strain, *Aeromonas hydrophila*, was selected to see how effectively the participants could differentiate between *Aeromonas* from *Vibrio spp.* Overall, 83% of the participating laboratories identified the strain correctly and thereby indicates that most laboratories are able to distinguish between *Vibrio* and *Aeromonas*.

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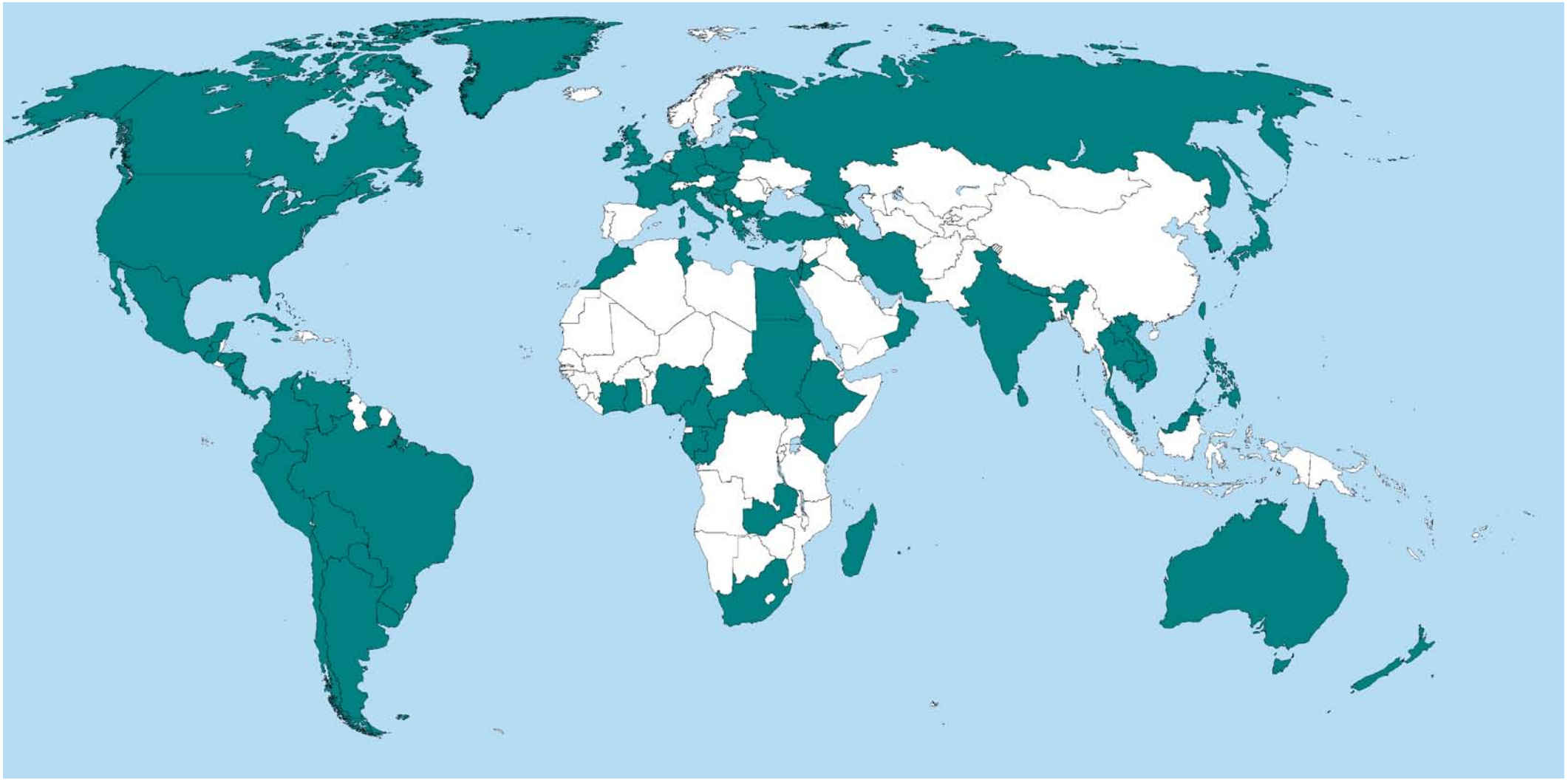
Figure and Tables

Figure 1. Countries participating* in the WHO EQAS 2011



*marked in green.

Table 1. EQAS participating laboratories' performance of *Salmonella* serotyping

EQAS iteration	Labs serotyping all provided strains		Correct test results	
	No.	**%**	**No.**	**%**
2000	34	92	165	76
2001	79	82	513	72
2002	80	81	668	91
2003	69	54	692	80
2004	78	61	701	81
2006	105	81	808	85
2007	109	78	920	88
2008	100	66	888	83
2009	119	83	974	86
2010	129	87	998	89
2011	109	89	878	92
Average	92	76	746	85

Table 2. Ability of EQAS participating laboratories to serotype the test *Salmonella* strains

Number of strains correctly serotyped	Participating laboratories											
	EQAS 2000		EQAS 2001		EQAS 2002		EQAS 2003		EQAS 2004		EQAS 2006	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
8	9	24	34	35	52	53	32	25	41	32	42	32
7	9	24	13	14	19	19	15	12	14	11	35	27
6	4	11	9	9	12	12	18	14	16	13	19	15
5	3	8	9	9	4	4	23	18	16	13	12	9
4	3	8	4	4	1	1	14	11	11	9	7	5
3	4	11	8	8	4	4	13	10	10	8	5	4
2	2	5	3	3	5	5	4	3	10	8	3	2
1	2	5	5	5	1	1	5	4	5	4	4	3
0	1	3	11	11	1	1	3	2	4	3	3	2
In total	37	100	96	100	99	100	127	100	127	100	130	100
Number of strains correctly serotyped	**Participating laboratories**											
	EQAS 2007		EQAS 2008		EQAS 2009		EQAS 2010		EQAS 2011		AVERAGE EQAS 2000 - 2011	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
8	66	47	50	33	76	50	91	61	82	67	52	43
7	29	21	36	24	29	19	16	11	17	14	21	17
6	13	9	11	7	7	5	12	8	10	8	12	10
5	11	8	14	9	13	8	9	6	2	2	11	9
4	7	5	12	8	5	3	6	5	4	3	7	6
3	6	4	9	6	7	5	2	1	4	3	7	5
2	2	1	8	6	5	3	2	1	1	1	4	3
1	6	4	9	6	6	4	7	5	3	2	5	4
0	0	0	2	1	5	3	3	2	0	0	3	2
In total	140	100	151	100	153	100	148	100	123	100	121	100

Table 3. Region-based categorization of EQAS participants' performance of *Salmonella* serotyping

Region	EQAS iteration	No. of labs	No. of strains serotyped	% strains correctly serotyped	Countries participating in EQAS 2011
Africa	2001	6	37	73.0	Cameroon, Central African Republic, Congo, Rep. of, Ivory Coast, Madagascar, Mauritius, Morocco (2), South Africa, Tunisia
	2002	9	62	87.1	
	2003	11	70	71.4	
	2004	9	51	62.7	
	2006	16	95	71.6	
	2007	11	73	80.8	
	2008	10	71	49.3	
	2009	15	94	75.5	
	2010	13	83	67.5	
	2011	10	57	79.2	
Central Asia & Middle East	2001	10	60	50.0	Israel, Jordan, Oman
	2002	5	30	83.3	
	2003	5	35	54.3	
	2004	5	33	54.5	
	2006	5	35	74.3	
	2007	5	40	55.0	
	2008	5	34	61.8	
	2009	5	32	46.9	
	2010	5	22	75.9	
	2011	3	23	95.8	
Caribbean	2001	0	0	0	Barbados
	2002	0	0	0	
	2003	3	18	61.1	
	2004	2	8	87.5	
	2006	3	14	78.6	
	2007	2	9	77.8	
	2008	3	14	78.6	
	2009	3	12	83.3	
	2010	2	13	92.9	
	2011	1	7	87.5	
Europe	2001	43	323	80.5	Albania, Belgium, Bosnia and Herzegovina (2), Bulgaria (2), Croatia, Cyprus, Czech Republic, Denmark (2), Estonia, Finland, France, Germany, Greece (2), Hungary, Ireland, Italy (12), Lithuania, Luxembourg, Malta, Poland (3), Serbia, Slovakia, Slovenia, Turkey, United Kingdom
	2002	50	384	90.0	
	2003	60	401	84.8	
	2004	57	392	84.7	
	2006	52	403	86.4	
	2007	54	415	89.4	
	2008	50	379	82.3	
	2009	47	362	93.1	
	2010	45	332	94.1	
	2011	42	314	94.6	

Table 3 (continued).
Region-based categorization of EQAS participants' performance of *Salmonella* serotyping

Region	EQAS iteration	No. of labs	No. of strains serotyped	% strains correctly serotyped	Countries participating in EQAS 2011
North America	2001	4	32	87.5	Canada, United States of America
	2002	2	16	100.0	
	2003	6	41	95.1	
	2004	8	55	81.8	
	2006	10	80	96.3	
	2007	12	94	97.9	
	2008	11	84	95.2	
	2009	12	90	92.2	
	2010	13	103	100.0	
	2011	11	81	97.6	
Oceania	2001	4	30	100.0	Australia,New Zealand
	2002	6	43	93.0	
	2003	6	46	93.5	
	2004	5	38	97.4	
	2006	5	37	94.6	
	2007	4	32	100.0	
	2008	4	30	93.3	
	2009	4	32	96.9	
	2010	4	32	100.0	
	2011	4	32	100.0	
Russia	2001	1	8	12.5	Belarus, Georgia, Russia
	2002	1	8	62.5	
	2003	1	7	14.3	
	2004	4	26	69.2	
	2006	5	40	80.0	
	2007	8	51	80.4	
	2008	6	40	90.0	
	2009	7	49	91.8	
	2010	8	54	87.1	
	2011	7	48	87.3	
Latin America	2001	11	78	57.7	Cuba (2), Argentina (2), Brazil (2), Chile, Colombia (3), Costa Rica (2), Ecuador (2), Guatemala, Honduras, Nicaragua, Panama, Paraguay, Peru (2), Uruguay, Venezuela
	2002	11	82	87.8	
	2003	13	83	75.9	
	2004	15	88	79.5	
	2006	13	84	84.5	
	2007	15	107	88.8	
	2008	17	120	71.7	
	2009	21	150	77.3	
	2010	22	132	80.0	
	2011	23	144	83.7	

Table 3 (continued).
Region-based categorization of EQAS participants' performance of *Salmonella* serotyping

Region	EQAS iteration	No. of labs	No. of strains serotyped	% strains correctly serotyped	Countries participating in EQAS 2011
Southeast Asia	2001	15	113	54.0	Brunei Darussalam, Cambodia, Japan (2), Korea Rep. of (2), Lao P.´s Dem. Rep., Malaysia (3), Mexico, Philippines, Singapore, Sri Lanka, Taiwan, Thailand (8)
	2002	12	90	92.2	
	2003	15	100	81.0	
	2004	17	130	81.5	
	2006	15	117	84.6	
	2007	19	140	91.4	
	2008	18	125	81.6	
	2009	23	180	81.1	
	2010	24	172	90.5	
	2011	23	180	98.4	

Table 4. *Salmonella* serogroups (SG), serotypes (ST) and deviations (D), WHO EQAS 2011

Strain ID	Correct serotype		No. of labs reporting SG	% D_{SG}	No. of labs reporting ST	% D_{ST}	Deviating results (*)
WHO S-11.1	Muenchen (or Virginia)	6,8:d:1,2	141	1.4	126	5.6	Bsilla (2), Lindenburg (1), Manhattan (1), Newport (1), O:6,8 H: d,1,2][Z67] (1), Valdosta, (1)
WHO S-11.2	Westhampton	3,10:g,s,t:-	137	5.8	126	9.5	Senftenberg (5), Regent (2), Amsterdam (2) Lekke (1), London (1), groupe II (1)
WHO S-11.3	Haifa	4,12:z10:1,2	144	2.8	124	9.7	Saintpaul (3), Tokoin (2), Albert (1), Heidelberg (1), Huettwilen (1),Kisangani(1), Stanley (1), Tudu (1), Typhimurium (1)
WHO S-11.4	Derby	4,12:f,g:-	138	0.7	125	14.4	Agona(8), Hato (2), Salamae(II) (2), 1,4,12,27:g,t:- (1), Agona II (1), Bredeney (1), Budapest (1), Salmonella (1), Stanley (1),
WHO S-11.5	Havana	13,23:f,g:-	128	4.7	121	6.6	Dublin (2), Raus (2), Agbeni (1), Newyork (1), Okatie (1), Viridi (1)
WHO S-11.6	Onireke	3,10:d:1,7	137	3.6	123	8.9	Birmingham (2), Lekke (2), Shangani (2), Give (1), London (1), Ontario (1), Stormont (1), Weybridge (1)
WHO S-11.7	Enteritidis	9,12:g,m:-	141	1.4	130	1.5	Berta (1), Salamae(II) (1)
WHO S-11.8	Abaetetuba	11:k:1,5	127	3.9	119	10.1	Pretoria (6), Harburg (1), Nyanza (1), Poona (1), Remete (1), Straengnaes (1), Salamae(II) (1)

*number of participants reporting the specified deviating result

Table 5. EQAS participating laboratories' performance of internal quality control strain (WHO S-11.7, *Salmonella* Enteritidis) serotyping

EQAS iteration	**Labs serotyping *S.* Enteritidis correctly**	
	No.	**%**
2000	34	92
2001	64	84
2004	113	95
2006	116	94
2007	135	96
2008	139	96
2009	141	93
2010	138	97
2011	128	98
Average	112	95

Table 6. EQAS participating laboratories' performance of antimicrobial susceptibility testing of *Salmonella* strains

EQAS iteration	**No. of EQAS participating laboratories**	**% correct test results**	**% minor deviations** (S ↔ I or I ↔ R)^	**% major deviations** (S → R)^	**% very major deviations** (R→ S)^	**% critical deviations** (R→ S & S → R)^	**% total deviations** (S → R & R → S & S ↔ I or I ↔ R)^
2000	44	92	4	4	0	4	8
2001	108	91	6	2	1	3	9
2002	119	92	6	2	1	3	9
2003*	147	93	4	3	0	3	7
2004	152	93	4	2	1	3	7
2006	143	88	8	3	1	4	12
2007	143	93	4	2	1	3	7
2008	168	91	4	2	3	5	9
2009	153	94	3	2	1	3	6
2010	152	92	4	3	2	5	8
2011	127	91	4	2	3	5	9
Average*	132	92	5	2	1	4	8

*Data do not include one strain which may have lost resistance due to transport or storage stress
^S, susceptible; I, intermediate; R, resistant

Table 7. Antimicrobial susceptibility test results (number of R/I/S) for the EQAS 2011 *Salmonella* strains*

Strain	Antimicrobial^												
	AMP	**CTX**	**CAZ**	**CRO**	**CHL**	**CIP**	**GEN**	**NAL**	**STR**	**SMX**	**SXT**	**TET**	**TMP**
WHO S-11.1	7/1/**130**	4/2/**108**	3/0/**101**	4/0/**89**	1/0/**125**	2/0/**131**	3/0/**123**	1/1/**122**	**83**/0/4	**67**/0/1	3/0/**121**	**126**/0/1	2/0/**62**
WHO S-11.2	7/3/**128**	6/2/**106**	3/1/**100**	3/0/**90**	2/0/**122**	6/0/**128**	4/1/**119**	0/10/**115**	2/5/78	4/1/**62**	2/0/**121**	2/4/**122**	1/0/**60**
WHO S-11.3	5/4/**128**	5/0/**109**	3/2/**98**	2/1/**89**	1/0/**123**	**74**/3/56	6/1/**118**	**123**/1/1	7/**22**/55	**67**/0/1	**121**/0/3	**126**/0/2	**61**/0/0
WHO S-11.4	**137**/0/1	6/4/**103**	8/2/**93**	5/2/**87**	2/1/**121**	**59**/2/73	5/0/**119**	6/27/**91**	5/**22**/57	3/2/**63**	4/0/**120**	**126**/0/2	1/0/**61**
WHO S-11.5	**132**/0/6	**110**/1/4	**99**/1/5	**87**/0/7	**116**/0/7	4/0/**131**	**108**/2/15	2/1/**122**	**77**/2/8	**63**/1/4	**112**/1/10	**59**/40/28	**59**/0/3
WHO S-11.6	**136**/0/1	5/0/**109**	2/0/**102**	0/0/**93**	1/0/**122**	**77**/7/51	4/0/**121**	58/32/**33**	1/**17**/66	2/2/**64**	2/0/**121**	1/2/**124**	0/0/**62**
WHO S-11.7	19/3/**115**	6/3/**104**	4/1/**98**	1/0/**92**	1/3/**119**	13/0/**121**	**125**/0/1	3/3/**118**	**80**/1/7	**67**/0/1	2/0/**122**	8/5/**115**	0/1/**59**
WHO S-11.8	6/1/**129**	2/1/**109**	0/1/**102**	1/0/**91**	0/0/**121**	4/0/**128**	4/0/**120**	1/3/**119**	3/**16**/64	3/3/**61**	1/0/**122**	0/4/**120**	0/0/**61**

^For antimicrobial abbreviations: see List of Abbreviations page 1

*In bold: expected interpretation. Grey cell: <90% of laboratories did correct interpretation. R, resistant/I, intermediate/ S, susceptible.

Table 8. EQAS participants' performance of *Salmonella* strains antimicrobial susceptibility testing categorized by antimicrobial

EQAS iteration	No. of labs	Performance	Antimicrobial[∞]																	
			AMC	AMP	CAZ	CHL	CIP	POD	CRO	CTX	GEN	KAN	NAL	SMX	STR	SXT	TET	TMP	XNL	OVERALL
2000	44	No. of tests	-	343	-	343	334	-			343	312	328	248	312	-	335	295	-	3,193
		% critical deviations*	-	6	-	4	1	-			4	4	1	3	4	-	6	1	-	3
		% total deviations^	-	8	-	7	6	-			5	16	4	5	12	-	13	1	-	8
2001	108	No. of tests	-	822	-	814	813	-			821	623	726	431	679	757	804	416	-	7,706
		% critical deviations*	-	4	-	2	1	-			2	2	2	6	7	2	7	1	-	3
		% total deviations^	-	7	-	3	4	-			4	7	8	9	27	5	18	2	-	9
2002	119	No. of tests	-	918	-	903	911	-			905	680	885	495	718	724	861	499	-	8,499
		% critical deviations*	-	2	-	2	0	-			2	2	2	4	4	7	3	3	-	3
		% total deviations^	-	3	-	3	2	-			16	10	4	4	34	10	7	3	-	9
2003•	147	No. of tests	-	1,019	-	996	995	-			993	738	947	615	768	929	995	582	-	9,577
		% critical deviations*	-	2	-	1	0	-			2	2	1	4	9	2	4	1	-	3
		% total deviations^	-	4	-	2	1	-			2	6	4	5	39	2	11	1	-	7
2004	152	No. of tests	973	1,178	-	1,159	1,162	-	-	995	1,201	-	1,130	734	947	1051	1,122	729	-	12,381
		% critical deviations*	6	3	-	2	0	-	-	0	2	-	1	5	1	3	5	2	-	3
		% total deviations^	12	5	-	2	1	-	-	14	3	-	4	8	21	4	11	2	-	7
2006	143	No. of tests	950	1,092	769	1,060	1,110	305	-	956	1,078	-	1,035	649	896	996	1,054	607	225	12,782
		% critical deviations*	9	2	7	3	2	1	-	7	3	-	2	6	5	3	9	1	2	4
		% total deviations^	22	3	11	15	6	26	-	15	7	-	6	7	22	5	20	2	9	12
2007	143	No. of tests	908	1,114	830	1,105	1,101	389	-	914	1,111	-	1,092	678	875	971	1,047	583	258	12,976
		% critical deviations*	6	5	1	0	1	4	-	1	3	-	2	5	4	3	4	1	0	3
		% total deviations^	17	7	1	6	1	16	-	2	4	-	3	6	26	3	11	2	6	7
2008	168	No. of tests	-	1,331	961	1,226	1,307	-	791	1,104	1,265	-	1,168	718	867	1,155	1,249	696	-	13,858
		% critical deviations*	-	3	3	1	19	-	3	3	4	-	2	4	7	3	6	2	-	5
		% total deviations^	-	8	6	11	21	-	6	6	6	-	4	5	25	4	13	2	-	9
2009	153	No. of tests	-	1,206	921	1,108	1,190	-	775	1,009	1,143	-	1,095	624	864	1,042	1,114	616	-	12,707
		% critical deviations*	-	3	1	1	8	-	0	1	2	-	1	7	9	3	4	1	-	3
		% total deviations^	-	6	1	2	10	-	1	2	3	-	3	9	30	4	10	1	-	6
2010	152	No. of tests	-	1,173	937	1,118	1,194	-	787	1,026	1,133	-	1,096	566	800	1,012	1,134	604	-	12,580
		% critical deviations*	-	4	2	1	3	-	4	4	5	-	1	14	19	4	5	1	-	5
		% total deviations^	-	5	3	2	3	-	8	8	6	-	2	17	55	4	9	1	-	9

Table 8 (continued). EQAS participants' performance of *Salmonella* strains antimicrobial susceptibility testing categorized by antimicrobial.

EQAS iteration	No. of labs	Performance	Antimicrobial[∞]																
			AMC	AMP	CAZ	CHL	CIP	POD	CRO	CTX	GEN	KAN	NAL	SMX	STR	SXT	TET	TMP	XNL	OVERALL
2011	127	No. of tests	-	1099	829	988	1070	-	744	909	999	-	993	542	682	988	1017	493	-	11353
		% critical deviations*	-	5	3	2	20	-	3	4	4	-	7	4	3	3	4	1	-	5
		% total deviations^	-	6	4	2	21	-	3	6	5	-	15	5	42	3	10	2	-	9
Average•	133	No. of tests	944	1027	875	984	1017	347	774	988	999	588	954	573	764	963	976	556	242	798
		% critical deviations*	7	4	3	2	5	3	3	3	3	3	2	6	7	3	5	1	1	4
		% total deviations^	17	6	4	5	7	21	5	8	6	10	5	7	30	4	12	2	8	9

Legend Figure 8

[∞]For antimicrobial abbreviations: see List of Abbreviations page 1

*R→ S & S → R (R, resistant; S, susceptible)

^S→R & R→S & S↔I or I↔R (I, intermediate)

• Data do not include one strain which may have lost resistance due to transport or storage stress

-, not determined

Table 9. Region-based categorization of EQAS participants' performance of *Salmonella* antimicrobial susceptibility testing

Region	EQAS iteration	No. of labs	% correct test result	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2011 iteration
Africa	2001	7	80.1	9.6	7.7	2.5	10.2	19.8	Cameroon, Central African, Republic Congo, Rep. Of, Ivory Coast, Ghana, Kenya, Madagascar, Mauritius, Morocco (2), Nigeria (2), Seychelles, South Africa, Sudan, Tunisia, Zambia
	2002	10	94.3	4.1	1.0	0.6	1.6	5.7	
	2003	13	86.9	6.6	2.8	3.7	6.5	13.1	
	2004	11	85.7	7.2	5.2	1.9	7.1	14.3	
	2006	20	85.8	7.5	4.1	2.7	6.8	14.3	
	2007	16	90,7	4.4	4.0	0.9	4.9	9.3	
	2008	19	83.8	6.5	5.5	4.2	9.7	16.2	
	2009	22	90.1	4.5	3.6	1.8	5.4	9.9	
	2010	22	84.7	6.0	6.5	2.8	9.3	15.3	
	2011	17	87.0	5.0	4.7	3.3	8.0	13.0	
Central Asia & Middle East	2001	10	87.7	6.3	5.2	0.8	6.0	12.3	Iran Islamic Republic of, Israel, Jordan, Oman
	2002	6	83.4	9.8	6.6	0.2	6.8	16.6	
	2003	8	89.9	4.5	4.0	1.6	5.6	10.1	
	2004	10	87.5	6.7	5.5	0.3	5.8	12.5	
	2006	7	79.2	10.5	9.8	0.5	10.3	20.8	
	2007	8	87.8	5.0	6.2	1.1	7.3	12.2	
	2008	12	86.1	6.5	4.0	3.4	7.4	13.9	
	2009	6	93.7	4.3	0.9	1.1	2.0	6.3	
	2010	7	95.8	2.6	0.2	1.4	1.6	4.2	
	2011	4	91.8	4.1	1.8	2.3	4.1	8.2	
Caribbean	2001	2	83.5	9.5	7.0	0.0	7.0	16.5	Barbados, Jamaica
	2002	1	95.8	4.2	0.0	0.0	0.0	4.2	
	2003	8	91.7	6.4	1.5	0.5	2.0	8.4	
	2004	8	94.1	3.1	1.9	0.9	2.8	5.9	
	2006	5	92.1	5.4	1.6	1.0	2.6	8.0	
	2007	4	95.0	3.1	0.9	0.9	1.8	5.0	
	2008	5	90.7	5.5	0.9	2.9	3.8	9.3	
	2009	4	93.2	1.8	3.2	1.8	5.0	6.8	
	2010	4	90.9	5.4	2.7	0.7	3.4	8.8	
	2011	2	96.5	1.4	0.0	2.1	2.1	3.5	
Europe	2001	47	91.3	5.7	2.7	0.3	3.0	8.7	Albania, Belgium, Bosnia and Herzegovina (2), Bulgaria (2), Croatia, Denmark (2), Estonia, Finland, France, Greece (2), Hungary, Ireland, Italy (9), Lithuania, Luxembourg, Malta, Poland (3), Serbia, Slovakia, Slovenia, Turkey, United Kingdom
	2002	57	92.7	5.2	1.2	0.9	2.1	7.3	
	2003	64	92.9	3.8	1.0	2.3	3.3	7.1	
	2004	58	93.5	4.3	1.4	0.8	2.2	6.5	
	2006	54	88.7	7.0	3.8	0.6	4.4	11.3	
	2007	49	94.2	3.7	1.6	0.4	2.0	5.7	
	2008	51	91.2	4.4	2.5	1.9	4.4	8.8	
	2009	40	95.1	2.6	1.3	0.9	2.2	4.8	
	2010	39	92.4	4.1	1.2	2.3	3.5	7.6	
	2011	36	92.5	4.5	1.7	1.3	3.0	7.5	

Table 9 (continued). Region-based categorization of EQAS participants' performance of *Salmonella* antimicrobial susceptibility testing

Region	EQAS iteration	No. of labs	% correct test result	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2011 iteration
North America	2001	4	95.8	3.8	0.0	0.4	0.4	4.2	Canada (5), United States of America (4)
	2002	3	90.5	6.9	0.6	2.0	2.6	9.5	
	2003	7	93.4	5.2	0.0	1.4	1.4	6.6	
	2004	9	94.2	4,2	1.8	0.0	1.8	6.0	
	2006	8	94.8	2.9	1.0	1.3	2.3	5.2	
	2007	10	95.4	2.9	0.8	0.8	1.6	4.6	
	2008	14	96.4	0.6	0.4	2.6	3.0	3.6	
	2009	10	98.7	0.0	0.4	0.9	1.3	1.3	
	2010	11	94.8	2.6	0.2	2.4	2.6	5.2	
	2011	9	92.1	2.6	1.5	3.8	5.3	7.9	
Oceania	2001	6	91.8	4.7	2.7	0.9	3.6	8.2	Australia (3), New Zealand
	2002	7	91.7	6.2	0.0	2.0	2.0	8.3	
	2003	9	94.3	2.5	1.2	2.0	3.2	5.7	
	2004	11	97.1	2.5	0.3	0.1	0.4	2.9	
	2006	7	93.4	4.6	0.9	1.1	2.0	6.6	
	2007	1	98.9	1.1	0.0	0.0	0.0	1.1	
	2008	4	93.9	3.8	0.0	2.3	2.3	6.1	
	2009	4	95.9	3.2	0.3	0.6	0.9	4.1	
	2010	4	92.5	4.6	0.6	2.3	2.9	7.5	
	2011	4	93.8	5.6	0.6	0.0	0.6	6.2	
Russia	2001	1	81,9	15,3	2,8	0.0	2.8	18.1	Belarus, Georgia, Russian Federation (5)
	2002	1	84,5	9,9	5,6	0.0	5.6	15.5	
	2003	1	100.0	0.0	0.0	0.0	0.0	0.0	
	2004	4	91.2	6.6	1.5	0.7	2.2	8.8	
	2006	5	87.4	8.2	2.7	1.7	4.4	12.6	
	2007	8	88.9	5.8	4.8	0.4	5.2	11.0	
	2008	6	92.2	4.7	1.4	1.7	3.1	7.8	
	2009	6	93.8	2.1	3.3	0.8	4.1	6.2	
	2010	8	94.3	3.3	1.3	1.1	2.4	5.7	
	2011	7	90.0	4.8	3.2	2.0	5.2	10.0	
Latin America	2001	11	90.8	6.9	1.4	1.0	2.4	9.2	Argentina, Belize, Brazil (2), Chile, Colombia (2), Costa Rica, Cuba, Ecuador (2), Guatemala (2), Honduras, Mexico, Nicaragua, Panama, Paraguay, Peru, Suriname, Uruguay, Venezuela
	2002	13	93.7	4.6	0.7	1.0	1.7	6.3	
	2003	12	90.8	4.2	2.0	3.0	5.0	9.2	
	2004	17	94.4	4.7	0.8	0.1	0.9	5.6	
	2006	16	88.7	6.3	4.5	0.6	5.1	11.3	
	2007	17	94.9	1.8	1.9	1.4	3.3	5.0	
	2008	20	93.0	3.4	1.5	2.1	3.6	7.0	
	2009	20	95.6	2.1	1.1	1.2	2.3	4.4	
	2010	23	90.8	2.1	5.6	1.4	7.1	9.2	
	2011	22	90,8	2,8	3,1	3,3	6.4	9,2	

Table 9 (continued). Region-based categorization of EQAS participants' performance of *Salmonella* antimicrobial susceptibility testing.

Region	EQAS iteration	No. of labs	% correct test result	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2011 iteration
Southeast Asia	2001	16	88.1	7.7	2.3	1.9	4.2	11.9	Brunei Darussalam, Cambodia, India (5), Japan (2), Korea Rep. Of (2), Lao P.´s Dem. Rep., Malaysia (4), Nepal, Philippines, Sri Lanka (2), Taiwan, Thailand (4), Viet Nam
	2002	18	89.0	8.1	1.4	1.6	3.0	11.0	
	2003	17	87.4	5.2	4.7	2.7	7.4	12.6	
	2004	16	92.8	4.4	2.3	0.5	2.8	7.2	
	2006	15	90.0	8.1	1.2	0.8	2.0	10.0	
	2007	20	93.9	4.0	1.4	0.7	2.1	6.1	
	2008	19	90.5	4.7	2.2	2.6	4.8	9.5	
	2009	27	91.8	4.1	3.0	1.2	4.2	8.3	
	2010	25	92.8	3.8	1.5	1.9	3.4	7.2	
	2011	26	90.5	3.5	2.4	3.5	5.9	9.5	

^S, susceptible; I, intermediate; R, resistant

Table 10. EQAS participants' performance of antimicrobial susceptibility testing of quality control strain *Escherichia coli* ATCC 25922

		Method	Labs' perfor-mance[5,6]	AMC	AMP	CAZ	CHL	CIP	POD	CRO	CTX	ENR[2]	FFN[2]	FIS (SMX)[3]	GEN	NAL	STR	SXT	TET	TMP	XNL[2]
Accepted interval[1]		**MIC (µg/ml)**		2-8	2-8	0.06-0.5	2-8	0.004-0.016	0.25-1	0.03-0.12	0.03-0.12	0.008-0.03	2-8	8-32	0.25-1	1-4	4-16[4]	≤0.5/9.5	0.5-2	0.5-2	0.25-1
		Disks (mm)		18-24	16-22	25-32	21-27	30-40	23-28	29-35	29-35	32-40	22-28	15-23	19-26	22-28	12-20	23-29	18-25	21-28	26-31
EQAS iteration (total no. of participants)	**2000** (44)	MIC & Disk	No.[5]	-	37	-	38	35	-	-	-	-	-	19	39	37	36	-	42	31	-
			%[6]	-	27	-	37	20	-	-	-	-	-	53	23	35	22	-	42	30	-
	2001 (107)	MIC & Disk	No.[5]	-	97	-	97	97	-	-	-	-	-	53	99	74	81	90	96	50	-
			%[6]	-	19	-	20	14	-	-	-	-	-	34	12	14	12	14	22	22	-
	2002 (114)	MIC & Disk	No.[5]	-	109	-	107	108	-	-	-	-	-	57	108	102	82	102	102	66	-
			%[6]	-	16	-	15	14	-	-	-	-	-	26	12	14	11	12	13	11	-
	2003 (144)	MIC & Disk	No.[5]	-	140	-	137	138	-	-	-	-	-	82	138	132	105	129	137	79	-
			%[6]	-	14	-	22	9	-	-	-	-	-	17	9	16	9	14	19	14	-
	2004 (140)	MIC & Disk	No.[5]	117	132	-	128	132	-	-	111	-	-	84	134	126	110	120	129	87	-
			%[6]	13	10	-	13	8	-	-	18	-	-	16	10	9	6	11	13	9	-
	2006 (137)	MIC & Disk	No.[5]	116	133	96	126	127	39	-	115	19	-	74	131	122	106	122	125	74	32
			%[6]	9	14	15	18	8	12	-	21	63	-	29	14	20	11	19	12	17	22
	2007 (126)	MIC & Disk	No.[5]	102	124	92	123	121	47	-	104	-	13	64	124	120	97	107	117	67	35
			%[6]	8	11	9	14	12	9	-	16	-	0	22	6	7	6	13	7	10	11
	2008 (147)	MIC & Disk	No.[5]	-	147	111	135	144	-	-	124	-	-	71	145	136	101	129	139	79	-
			%[6]	-	12	9	10	8	-	-	14	-	-	14	8	8	12	13	7	13	-
		MIC	No.[5]	-	33	23	24	33	-	-	23	-	-	18	31	23	19	22	28	16	-
			%[6]	-	0	5	0	6	-	-	9	-	-	11	0	0	11	9	0	13	-
		Disk	No.[5]	-	114	89	112	111	-	-	101	-	-	53	114	113	82	107	111	63	-
			%[6]	-	16	10	12	8	-	-	15	-	-	15	11	10	12	14	9	13	-
	2009 (129)	MIC & Disk	No.[5]	-	128	100	121	124	-	88	107	-	-	63	123	117	98	113	122	70	-
			%[6]	-	16	13	15	7	-	16	10	-	-	11	18	13	10	14	14	11	-
		MIC	No.[5]	-	27	19	24	26	-	20	20	-	-	14	25	24	19	21	27	25	-
			%[6]	-	11	11	8	8	-	15	15	-	-	21	12	8	5	19	11	13	-
		Disk	No.[5]	-	101	81	97	98	-	68	87	-	-	49	98	93	79	92	95	55	-
			%[6]	-	16	14	16	6	-	16	9	-	-	10	18	14	11	12	15	11	-
	2010 (116)	MIC & Disk	No.[5]	-	114	97	108	115	-	79	100	-	-	51	112	104	84	101	110	63	-
			%[6]	-	11	9	9	6	-	10	14	-	-	11	11	5	5	12	5	15	-
		MIC	No.[5]	-	25	15	21	25	-	15	17	-	-	12	24	19	17	17	24	11	-
			%[6]	-	12	20	10	8	-	7	18	-	-	8	13	16	18	18	17	36	-
		Disk	No.[5]	-	89	82	87	90	-	64	83	-	-	39	88	85	67	84	86	52	-
			%[6]	-	9	6	8	4	-	9	11	-	-	10	9	2	1	10	1	8	-
	2011 (111)	MIC & Disk	No.[5]	-	111	89	102	109	-	76	96	-	-	50	103	103	72	99	107	51	-
			%[6]	-	17	4	11	7	-	7	9	-	-	8	11	8	4	16	7	14	-
		MIC	No.[5]	-	23	15	18	22	-	16	15	-	-	13	22	19	17	16	21	11	-
			%[6]	-	4	7	0	9	-	6	0	-	-	8	9	0	6	6	5	0	-
		Disk	No.[5]	-	88	74	84	87	-	60	81	-	-	37	81	84	55	83	86	40	-
			%[6]	-	20	4	13	7	-	7	11	-	-	8	11	10	4	18	8	18	-

Legend table 10

[0]For antimicrobial abbreviations: see List of Abbreviations page 1
[1]CLSI standard, Performance Standards for Antimicrobial Disk and Dilution Susceptibility testing. 21th Informational supplement. CLSI document M100-S21, Wayne, Pennsylvania
[2]CLSI standard, Performance Standards for Antimicrobial Disk and Dilution Susceptibility Tests for bacteria Isolated from Animals. M31-A3. 3rd Edition[Approved Standard]. 2008. Wayne, PA, USA
[3]FIS (sulfisoxazole) covers the group of SMX (sulfonamides)
[4]Quality control range developed by the manufacturer of Sensititre®
[5]No., number of labs performing the analysis
[6]%, percentage of labs reporting erroneous results
-, not determined

Table 11. *Shigella* serotypes (ST) and deviations (D), WHO EQAS 2011

Strain	Correct serotype	No. of labs reporting correct identification	D (%)	Deviating results (*)	No. of labs reporting correct ST	D (%)	Deviating results (*)
WHO SH-11.1	*S. flexneri* serotype 6	104	2.8	3	66	5,7	4a (2), 3 (1), 1b (1)
WHO SH-11.2	*S. sonnei*	105	2.8	3	N/A	N/A	N/A
WHO SH-11.3	*S. boydii* serotype 2	102	1.9	2	48	5,9	1 (1), 11 (1), 14 (1)
WHO SH-11.4	*S. flexneri* serotype 1b	109	0.9	1	53	11,7	1a (6), 3a (1)

*number of participants reporting deviating result

Table 12. Region-based categorization of laboratories performing *Shigella* serotyping in 2011

Region	Year	No. of laboratories	No. of strains serotyped	Strains serotyped correctly (%)	Countries participating in the 2011 iteration
Africa	2009	8	18	72.2	Kenya, Mauritius, South Africa, Tunisia
	2010	7	16	62.5	
	2011	4	10	100.0	
Central Asia & Middle East	2009	3	5	100.0	Israel, Oman
	2010	3	6	83.3	
	2011	2	6	100.0	
Europe	2009	15	40	92.5	Albania, Belgium, Bosnia and Herzegovina, Bulgaria, Czech Republic, Denmark, Finland, Germany, Greece, Ireland, Italy, Lithuania, Luxembourg, Malta, Serbia, Slovenia, Turkey, United Kingdom
	2010	15	35	85.7	
	2011	16	42	92.9	
North America	2009	7	18	100.0	Canada (4), United States of America (2)
	2010	7	20	100.0	
	2011	6	16	100.0	
Oceanic	2009	3	8	100.0	Australia, New Zealand
	2010	3	8	100.0	
	2011	3	8	100.0	
Russia	2009	6	18	83.3	Belarus, Georgia, Russian Federation (4)
	2010	7	20	75.0	
	2011	6	18	88.9	
Latin America	2009	16	40	97.5	Argentina, Brazil (2), Chile, Colombia, Costa Rica, Cuba, Ecuador, Mexico, Nicaragua, Panama, Paraguay, Peru, Uruguay, Venezuela
	2010	13	33	78.8	
	2011	15	37	94.6	
Southeast Asia	2009	11	30	90.0	Japan (2), Korea Rep. of, Lao P.´s Dem. Rep., Malaysia, Seychelles, Sri Lanka, Taiwan, Thailand (5)
	2010	14	32	87.5	
	2011	13	33	84.8	

Table 13. EQAS participating laboratories' performance of *Shigella* strains antimicrobial susceptibility testing

EQAS iteration	No. of participating laboratories	% correct test results	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S → R & R → S & S ↔ I or I ↔ R)^
2008	15	95	2	2	1	3	5
2009	111	96	2	1	1	2	4
2010	114	91	2	1	6	7	9
2011	107	92	2	1	4	5	7

^S, susceptible; I, intermediate; R, resistant

Table 14. Antimicrobial susceptibility test results (number of R/I/S) for the EQAS 2011 *Shigella* strains*

Strain	Antimicrobial∞												
	AMP	**CTX**	**CAZ**	**CRO**	**CHL**	**CIP**	**GEN**	**NAL**	**STR**	**SMX**	**SXT**	**TET**	**TMP**
WHO SH-11.1	9/4/**86**	2/0/**83**	1/0/**78**	0/0/**69**	1/0/**85**	3/0/**95**	2/0/**87**	1/1/**89**	2/17/**40**	0/0/**46**	2/0/**88**	2/2/**87**	2/0/**43**
WHO SH-11.2	**98**/0/1	**83**/0/1	**64**/9/7	**71**/0/1	3/0/**86**	**40**/1/56	4/0/**84**	**87**/1/3	**58**/0/3	**42**/0/1	**88**/0/2	**89**/0/3	**44**/0/0
WHO SH-11.3	11/5/**86**	3/0/**84**	2/0/**80**	1/0/**72**	0/0/**89**	**49**/2/50	4/2/**86**	**88**/3/3	**62**/0/1	**44**/0/1	**90**/0/5	4/1/**91**	**43**/0/2
WHO SH-11.4	**102**/0/1	**84**/0/3	**61**/13/7	**71**/0/4	**78**/7/4	**51**/4/45	2/2/**86**	8/21/**64**	**60**/0/3	**44**/0/1	**93**/03	**96**/0/1	**44**/0/0

∞For antimicrobial abbreviations: see List of Abbreviations page 1

*In bold: expected interpretation. Grey cell: <90% of laboratories did correct interpretation. R, resistant; I, intermediate; S, susceptible.

Table 15. EQAS laboratories' performance of *Shigella* strains antimicrobial susceptibility testing categorized by antimicrobial

EQAS iteration	No. of labs	Lab performance	Antimicrobial													
			AMP	**CAZ**	**CHL**	**CIP**	**CTX**	**GEN**	**NAL**	**SMX**	**STR**	**SXT**	**TET**	**TMP**	**CRO**	**OVERALL**
2008	15	No. of tests	52	44	51	48	48	50	52	7	27	52	52	4	42	529
		% critical deviations*****	1	2	1	-	2	1	-	-	4	2	4	-	2	1.5
		% total deviations^	1	2	1	-	2	1	-	-	9	2	8	-	2	2.2
2009	111	No. of tests	423	358	388	426	372	396	388	211	293	388	386	218	301	4548
		% critical deviations*****	2.4	0.3	2.1	0.2	1.1	2.5	0.5	3.8	5.8	2.3	2.8	1.8	0.3	1.9
		% total deviations^	3.8	0.3	4.6	0.9	1.1	3.5	1.5	3.8	18.1	3.6	7.5	1.8	0.6	3.8
2010	114	No. of tests	424	344	402	434	377	403	382	194	275	363	410	218	291	4517
		% critical deviations*	1.7	0.6	3.5	40.8	2.4	3.5	2.1	4.6	8.0	8.3	4.4	3.7	0.0	6.4
		% total deviations^	1.9	1.2	9.2	77.9	3.0	5.5	3.0	6.0	14.6	13.8	5.9	3.8	0.0	11.2
2011	107	No. of tests	403	322	353	396	343	359	369	179	246	371	376	178	289	
		% critical deviations*	5.5	5.2	2.2	38.9	2.7	3.3	4.0	1.7	3.6	3.2	2.7	2.2	2.0	5.5
		% total deviations^	7.7	12.0	4.2	40.7	2.7	4.4	11.0	1.7	10.5	3.2	3.5	2.2	2.0	7.7

∞For antimicrobial abbreviations: see List of Abbreviations page 1

*****R→ S & S → R (R, resistant; S, susceptible)

^S→R & R→S & S↔I or I↔R (I, intermediate)

-, not determined

Table 16. Region-based categorization of EQAS participating laboratories' performance of antimicrobial susceptibility tests for *Shigella* strains in 2011

Region	Year	No. of labs	% correct test result	% minor deviations (S↔I or I↔R)^	% major deviations (S→R)^	% very major deviations (R→ S)^	% critical deviations (R→ S & S → R)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2011 iteration
Africa	2009	17	93.3	2.4	3.5	0.8	4.3	6.8	Cameroon, Central African Republic, Congo, Rep. of, Ivory Coast, Ghana, Kenya, Madagascar, Mauritius, Morocco, Nigeria (2), Seychelles, South Africa, Sudan, Tunisia,Zambia
	2010	16	84.8	2.5	2.7	10.0	12.7	15.2	
	2011	16	86.0	1.8	3.6	8.3	11.9	13.7	
Central Asia & Middle East	2009	5	94.8	0.9	3.0	1.3	4.4	5.2	Jordan, Iran, Israel, Oman
	2010	6	90.6	1.2	1.6	6.7	8,3	9.4	
	2011	4	92.9	1.6	0.5	4.9	5.4	7.1	
Caribbean	2009	4	95.6	1.5	0.7	2.2	2.9	4.4	Barbados
	2010	4	88.5	1.5	3.8	6.2	10.0	11.5	
	2011	1	97.7	2.3	0.0	0.0	2,3	2.3	
Europe	2009	22	98.1	1.1	0.7	0.1	0.8	1.9	Albania, Belgium, Bosnia and Herzegovina (2), Bulgaria, Denmark (2), Finland, Greece, Ireland, Italy (5), Lithuania, Luxembourg, Malta, Poland (2), Serbia, Slovenia, Turkey, United Kingdom
	2010	27	93.6	1.5	0.9	3.9	4.8	6.4	
	2011	24	94.8	2.2	0.5	2.5	3.0	5.1	
North America	2009	6	100.0	0.0	0.0	0.0	0.0	0.0	Canada, United States of America
	2010	7	95.0	0.0	0.0	5.0	5.0	5.0	
	2011	4	90.1	0.7	3.3	5.9	9,2	9.9	
Oceanic	2009	-	-	-	-	-	-	-	Australia
	2010	1	90.0	10.0	0.0	0.0	0.0	10.0	
	2011	1	92.5	5.0	0.0	2.5	2.5	7.5	
Russia	2009	6	95.5	1.6	1.6	1.3	2.9	4.6	Belarus, Georgia, Russian Federation
	2010	7	92.1	2.9	1.5	3.5	5.0	7.9	
	2011	6	94.4	3.6	0.0	2.0	2.0	5.6	
Latin America	2009	20	98.3	1.1	0.4	0.3	0.7	1.7	Argentina, Belize, Brazil (2), Chile, Colombia, Costa Rica, Ecuador (2), Guatemala (2), Honduras, Mexico, Nicaragua, Panama, Paraguay, Peru, Suriname, Uruguay, Venezuela
	2010	22	92.1	1.3	2.1	4.5	6.6	7.9	
	2011	20	94.0	1.5	1.3	3.2	4.5	6.0	
Southeast Asia	2009	18	94.1	3.9	0.3	1.7	2.0	5.9	Cambodia, India (5), Japan (2), Korea Rep. Of, Lao P.´s Dem. Rep., Malaysia (2), Nepal, Philippines, Sri Lanka (2), Thailand (3)
	2010	16	90.5	2.4	0.7	6.4	7.1	9.5	
	2011	19	90.0	2.1	0.8	6.1	6.9	9.0	

^S, susceptible; I, intermediate; R, resistant.

Table 17. Proportion of laboratories that obtained the expected result. Number (n/N) and percentages of laboratories which correctly detected and confirmed the ESBL and non ESBL producing *Salmonella* and *Shigella* strains.

Isolate no.	Expected interpretation	Confirmatory tests	
		CAZ/CL:CAZ	CTX/CL:CTX
WHO S-11.1	non ESBL	17/17 (100%)	22/22 (100%)
WHO S-11.2	non ESBL	18/19 (95%)	22/24 (92%)
WHO S-11.3	non ESBL	17/18 (94%)	22/22 (100%)
WHO S-11.4	non ESBL	18/19 (95%)	22/23 (96%)
WHO S-11.5	ESBL	53/56 (95%)	58/63 (95%)
WHO S-11.6	non ESBL	17/17 (100%)	23/23 (100%)
WHO S-11.7	non ESBL	19/19 (100%)	23/23 (100%)
WHO S-11.8	non ESBL	16/17 (94%)	21/21 (100%)
WHO SH-11.1	non ESBL	12/12 (100%)	17/17 (100%)
WHO SH-11.2	ESBL	42/44 (95%)	46/50 (92%)
WHO SH-11.3	non ESBL	12/13 (92%)	17/17 (100%)
WHO SH-11.4	ESBL	42/43 (98%)	45/49 (92%)

Table 18. EQAS participating laboratories' performance of *Campylobacter* strains identification

EQAS iteration	No. of labs	Correct species	Strain no.	No. of results submitted	% correct identification	Deviating results (*)
2003	97	*C. jejuni*	# 1	92	87%	*C. coli* (9) *C. lari* (3)
	97	*C. coli*	# 2	92	83%	*C. jejuni* (7) *C. lari* (4) *C. upsaliensis* (4)
2004	109	*C. lari*	# 1	95	80%	*C. coli* (11) *C. jejuni* (8)
	109	*C. jejuni*	# 2	107	87%	*C. coli* (8) *C. lari* (4) *C. upsaliensis* (2)
2006	99	*C. jejuni*	# 1	86	90%	*C. lari* (3) *C. coli* (3) *C. upsaliensis* (3)
	99	*C. coli*	# 2	94	66%	*C. lari* (19) *C. jejuni* (11) *C. upsaliensis* (2)
2007	142	*C. lari*	# 1	95	72%	*C. jejuni* (10) *C. coli* (9) *C. upsaliensis* (7)
	142	*C. coli*	# 2	99	74%	*C. lari* (3) *C. jejuni* (20) *C. upsaliensis* (2)
2008	154	*C. lari*	# 1	105	63%	*C. coli* (14) *C. jejuni* (18) *C. upsaliensis* (7)
	154	*C. lari*	# 2	105	60%	*C. coli* (10) *C. jejuni* (19) *C. upsaliensis* (13)
2009	131	*C. coli*	# 1	87	77%	*C. upsaliensis* (10) *C. jejuni* (9) *C. lari* (1)
	131	*C. jejuni*	# 2	87	95%	*C. upsaliensis* (3) *C. lari* (1)
2010	130	*C. jejuni*	# 1	88	92%	*C. coli* (4) *C. lari* (3) *C. upsaliensis* (1)
	130	*C. coli*	# 2	84	85%	*C. jejuni* (11) *C. lari* (2) *C. upsaliensis* (2)
2011	132	*C. coli*	# 1	81	59%	*C. jejuni* (19) *C. lari* (13) *C. upsaliensis* (1)
	132	*C. coli*	# 2	79	70%	*C. jejuni* (17) *C. lari* (5) *C. upsaliensis* (2)

*number of participants reporting the specified deviating result

Table 19. Region-based categorization of EQAS 2011 participating laboratories' performance of *Campylobacter* strains identification

Region	Year	No. of labs	No. of strains identified	% strains correctly identified	Countries participating in the 2011 iteration
Africa	2009	8	13	54	Cameroon, Central African Republic, Ivory Coast, Kenya, Madagascar, Mauritius, South Africa, Sudan, Tunisia
	2010	7	13	77	
	2011	9	17	35	
Central Asia & Middle East	2009	3	5	40	Israel, Oman, Saudi Arabia
	2010	3	6	100	
	2011	2	2	50	
Caribbean	2009	2	4	100	Barbados
	2010	3	6	67	
	2011	1	2	0	
Europe	2009	28	53	89	Bulgaria, Cyprus, Czech Republic, Denmark (2), Estonia, Finland, Germany, Greece, Hungary, Italy (8), Lithuania, Luxembourg. Malta, Poland (2), Serbia, Turkey
	2010	29	57	96	
	2011	25	48	85	
North America	2009	10	19	90	Canada, United States of America
	2010	11	22	86	
	2011	9	18	78	
Oceania	2009	2	4	100	Australia, New Zealand
	2010	2	3	100	
	2011	2	4	100	
Russia	2009	2	4	100	Belarus, Georgia
	2010	2	4	100	
	2011	2	4	50	
Latin America	2009	14	26	89	Argentina (2), Brazil (2), Chile, Colombia (3), Costa Rica, Ecuador, Guatemala (2), Mexico, Paraguay, Peru (2), Uruguay, Venezuela (2)
	2010	19	37	78	
	2011	19	37	49	
Southeast Asia	2009	10	20	90	Brunei Darussalam, Cambodia, India, Japan, Korea Rep. Of, Lao P.´s Dem. Rep., Malaysia, Philippines, Taiwan, Thailand (3)
	2010	14	27	93	
	2011	12	24	67	

Table 20. EQAS participants' performance of *Campylobacter* strains antimicrobial susceptibility testing

EQAS iteration	No. of labs	% correct test results	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (R → S & S → R)^
2009	25	91.4	4.5	4.1	8.6
2010	37	91.3	4,2	4,5	8,7
2011	32	93,8	2,8	3,4	6.2

^S, susceptible; R, resistant

Table 21. Antimicrobial susceptibility test results (number of R/S) for the EQAS 2011 *Campylobacter* strains*

Strain	Antimicrobial^						
	CHL	**CIP**	**ERY**	**GEN**	**NAL**	**STR**	**TET**
WHO C-11.1	0/**21**	**32**/2	1/**30**	1/**31**	**28**/3	**14**/1	1/**29**
WHO C-11.2	0/**20**	2/**31**	**28**/3	1/**32**	2/**29**	3/**12**	**26**/4

^For antimicrobial abbreviations, see List of Abbreviations page 1

*In bold: expected interpretation. R, resistant; S, susceptible

Table 22. EQAS participants' performance of *Campylobacter* antimicrobial susceptibility testing categorized by antimicrobial

EQAS iteration	No. of labs	Lab performance	Antimicrobial						
			CHL	**CIP**	**ERY**	**GEN**	**NAL**	**STR**	**TET**
2009	25	No. of tests	37	46	46	43	41	34	45
		% critical deviations*	8.1	6.5	10.8	2.3	9.8	11.8	11.1
2010	37	No. of tests	44	70	71	59	53	39	68
		% critical deviations*	4.8	7.7	12.7	11.3	8.2	11.4	9.7
2011	32	No. of tests	41	67	62	65	62	30	60
		% critical deviations*	0.0	6.0	6.5	3.1	8.1	13.3	8.3

^For antimicrobial abbreviations, see List of Abbreviations page 1

*****R→ S & S → R (R, resistant; S, susceptible)

Table 23. Region-based categorization of EQAS 2011 participants' performance of antimicrobial susceptibility testing of *Campylobacter* strains

Region	Year	No. of labs	% correct test result	% major deviations (S → R)^	% very major deviations (S → R)^	% critical deviations (R→S & S→R)^	Countries participating in the 2011 iteration
Africa	2009	2	50.0	21.4	28.6	50.0	Cameroon, Central African Republic, Ivory Coast, Madagascar, Sudan, Tunisia
	2010	2	95.2	0.0	4.8	4.8	
	2011	6	82.7	3.8	13.5	17.3	
Central Asia & Middle East	2009	0	-	-	-	-	Iran
	2010	0	-	-	-	-	
	2011	1	75.0	0.0	25.0	25.0	
Europe	2009	9	98.3	1.7	0.0	1.7	Denmark (2), Greece, Hungary, Italy (3), Luxembourg, Malta, Poland (2)
	2010	13	100.0	0.0	0.0	0.0	
	2011	11	100.0	0.0	0.0	0.0	
North America	2009	2	100.0	0.0	0.0	0.0	Canada, United States of America.
	2010	5	93.8	6.3	0.0	6.3	
	2011	5	100.0	0.0	0.0	0.0	
Oceanic	2009	0	-	-	-	-	Australia
	2010	0	-	-	-	-	
	2011	1	100.0	0.0	0.0	0.0	
Russia	2009	0	-	-	-	-	Georgia
	2010	1	78.6	7.1	14.3	21.4	
	2011	1	100.0	0.0	0.0	0.0	
Latin America	2009	5	93.2	6.8	0.0	6.8	Argentina, Brazil, Chile, Costa Rica, Paraguay,Peru (2)
	2010	8	89.6	6.0	4.5	10.4	
	2011	7	96.8	0.0	3.2	3.2	
Southeast Asia	2009	4	71.4	0.0	28.6	28.6	Japan, Korea Rep. Of, Philippines, Thailand (2)
	2010	7	77.2	9.8	13.0	22.8	
	2011	5	85.1	9.0	6.0	15.0	

^S, susceptible; R, resistant

Table 24. EQAS 2011 participants' performance of antimicrobial susceptibility testing of *Campylobacter jejuni* ATCC 33560

	Method used	Incubation conditions	Labs' performance[1, 2]	Antimicrobial[3]					
				CHL	CIP	ERY	GEN	NAL	TET
EQAS 2010 (N=20)	Microdilution	42°C / 24h	No.[1]	3	6	6	6	4	6
			%[2]	67	83	100	83	75	83
	Microdilution	36-37°C / 48h	No.[1]	5	8	8	8	7	8
			%[2]	80	88	88	75	86	88
	Agardilution	42°C / 24h	No.[1]	0	6	6	6	0	0
			%[2]	0	100	83	83	0	0
	Agardilution	36-37°C / 48h	No.[1]	0	0	0	0	0	0
			%[2]	0	0	0	0	0	0
	Overall	Overall	No.[1]	8	20	20	20	11	14
			%[2]	75	90	90	80	82	86
EQAS 2011 (N=26)	Microdilution	42°C / 24h	No.[1]	4	9	9	8	7	9
			%[2]	100	67	100	88	100	67
	Microdilution	36-37°C / 48h	No.[1]	6	8	6	8	7	7
			%[2]	83	88	100	75	86	86
	Agardilution	42°C / 24h	No.[1]	-	8	8	8	-	-
			%[2]	-	88	63	100	-	-
	Agardilution	36-37°C / 48h	No.[1]	-	1	1	1	-	-
			%[2]	-	0	0	100	-	-
	Overall	Overall	No.[1]	10	26	24	25	14	16
			%[2]	90	77	83	88	93	75

[1]No., number of labs performing the analysis
[2]%, percentage of labs reporting correct results
[3]For antimicrobial abbreviations: see List of Abbreviations page 1
-, not determined

Table 25. EQAS participating laboratories' performance of unknown strain identification

EQAS iteration	Strain ID	No. of participating labs	Pecentage (%) of labs performing correct identification
2003	*E. coli* O157	115	99
2004	*Shigella flexneri*	121	94 (*Shigella)* 74 (*S. flexneri)*
2006	*Yersinia enterocolitica* O3	134	93 (*Yersinia)* 89 (*Y. enterocolitica)* 66 (*Y. enterocolitica* O3)
2007	*Vibrio parahaemolyticus*	86	83
2008	*Enterobacter sakasakii*	128	92
2009	*Vibrio mimicus*	56	48
2010	*Citrobacter spp.*	115	90
2011	*Aeromonas hydrophila*	106	83

Appendixes (1, 2, 3, 4a, 4b)

Appendix 1	Prenotification
Appendix 2	Expected results
Appendix 3	Protocol
Appendix 4a	Subculture and Maintenance of QC strains
Appendix 4b	Instructions for opening and reviving lyophlised cultures

DFVF- M00-06-001/21.05.2010

Lyngby, 14 April 2011

SIGN-UP FOR EQAS 2011

Greetings to the WHO Global Foodborne Infections Network (WHO GFN) Members:

WHO GFN strives to increase the quality of laboratory-based surveillance of *Salmonella* and other foodborne pathogens by encouraging national and regional reference laboratories that attended WHO GFN training courses to participate in the External Quality Assurance System (EQAS). The 2010 EQAS cycle is completed, and we are pleased to announce the launch of the 2011 EQAS cycle.

WHY PARTICIPATE IN EQAS?

EQAS provides the opportunity for proficiency testing which is considered an important tool for the production of reliable laboratory results of consistently good quality.

WHAT IS OFFERED IN EQAS?

This year, WHO EQAS offers the following components:

- serogrouping, serotyping and antimicrobial susceptibility testing of eight *Salmonella* isolates;
- serotyping and antimicrobial susceptibility testing of four *Shigella* isolates;
- species identification and antimicrobial susceptibility testing of two *Campylobacter* isolates;
- identification of one unknown bacterial isolate.

WHO SHOULD PARTICIPATE IN EQAS 2011?

All national and regional reference laboratories which perform analysis on *Salmonella*, *Shigella* and/or *Campylobacter* and are interested in performing quality assurance are invited to participate. We expect that all national and regional reference laboratories that attended WHO GFN Training Courses will participate in EQAS.
The WHO GFN Regional Centers in cooperation with the EQAS Coordinator will evaluate the list of laboratories that sign-up for EQAS 2011. Laboratories which signed-up and received bacterial isolates in year 2010 but did not submit any result should provide a consistent explanation if they want to participate in 2011.

COST FOR PARTICIPATING IN EQAS

There is no participation fee in EQAS 2011. However, laboratories should cover the expenses for parcel shipment if they can afford it. If your country has an agreement with FedEx regarding import of Biological Substance Category B (UN3373), please provide your FedEx import account number in the sign-up form or, alternatively, to the EQAS Coordinator (please find contact information below). We need this information at this stage to save time and resources. Participating laboratories are responsible for paying any expenses related to taxes or custom fees applied by their country.

HOW TO SIGN- UP FOR EQAS 2011

This link will open a sign-up webpage: http://thor.dfvf.dk/signup

In this webpage, you will be asked to provide the following information:

- Name of institute, department, laboratory and contact person
- Complete mailing address for shipment of bacterial isolates (no post-office box number)
- Telephone and fax number, E-mail address
- FedEx import account number (if available)
- Approximate number of *Salmonella* isolates annually serogrouped/serotyped
- Approximate number of *Salmonella* isolates annually tested for antimicrobial susceptibility
- Availability of ATCC reference strains
- Components of EQAS 2011you plan to perform (level of participation)
- Level of reference function in your country

If you experience any problem in the sign-up webpage, please try again a few days later. If problems persist after several attempts, please contact the EQAS Coordinator Susanne Karlsmose: E-mail suska@food.dtu.dk; fax +45 3588 6341.

TIMELINE FOR SHIPMENT OF ISOLATES AND AVAILABILITY OF PROTOCOLS

Due to increased number of participants in WHO EQAS, a number of different institutions will ship the bacterial isolates, and you will receive information concerning the institution shipping your parcel. The bacterial isolates will be shipped between August and September 2011.

In order to minimize delays, **please send a valid import permission to the EQAS coordinator**. Please apply for a permit to receive the following (according to your level of participation): "Biological Substance Category B": eight *Salmonella* strains, four *Shigella* strains, two *Campylobacter*, one *Campylobacter* reference strain (for new participants performing antimicrobial susceptibility testing on *Campylobacter*), one *Escherichia coli* reference strain (for new participants performing antimicrobial susceptibility testing on *Salmonella* and/or *Shigella*) and an unknown sample (enteric bacteria) between August and September 2011.

Protocols and all relevant information will be available for download from the website http://www.antimicrobialresistance.dk/233-169-215-eqas.htm.

DEADLINE FOR SUBMITTING RESULTS TO THE NATIONAL FOOD INSTITUTE

Results must be submitted to the National Food Institute (DTU Food) by **31st December 2011** through the password-protected website. An evaluation report will be generated upon submission of results. Full anonymity is ensured, and only DTU Food and the WHO GFN Regional Centre in your region will have access to your results.

Deadline for sign-up for EQAS 2011 is 30th May 2011

			Ampicillin		Cefotaxime		Ceftazidime		Ceftriaxone		Chloramphenicol		Ciprofloxacin		Gentamicin		Nalidixic acid		Streptomycin		Sulfonamides		Tetracycline		Trimethoprim		Trim/Sulfa		
			AMP		**CTX**		**CAZ**		**CRO**		**CHL**		**CIP**		**GEN**		**NAL**		**STR**		**SMX**		**TET**		**TMP**		**SXT**		
WHO 2011 S-11.1	*Salmonella* Muenchen	6,8:d:1,2	<= 1	SUSC	= 0.25	SUSC	= 0.5	SUSC	= 0.125	SUSC	= 4	SUSC	= 0.03	SUSC	= 1	SUSC	<= 4	SUSC	> 128	RES	> 1024	RES	> 32	RES	<= 1	SUSC	= 0.125	SUSC	
WHO 2011 S-11.2	*Salmonella* Westhampton	3,10:g,s,t:-	<= 1	SUSC	<= 0.12	SUSC	= 0.5	SUSC	= 0.09	SUSC	= 8	SUSC	= 0.06	SUSC	<= 0.5	SUSC	= 8	SUSC	<= 8	SUSC	<= 64	SUSC	<= 2	SUSC	<= 1	SUSC	= 0.09	SUSC	
WHO 2011 S-11.3	*Salmonella* Haifa	4,12:z10:1,2	= 2	SUSC	<= 0.12	SUSC	= 1	SUSC	<= 0.25	SUSC	= 8	SUSC	= 0.5	RES	= 2	SUSC	> 64	RES	= 16	INTERM	> 1024	RES	> 32	RES	> 32	RES	> 32	RES	
WHO 2011 S-11.4	*Salmonella* Derby	4,12:f,g:-	> 32	RES	<= 0.12	SUSC	= 1	SUSC	= 0.064	SUSC	= 4	SUSC	= 0.5	RES	<= 0.5	SUSC	= 8	SUSC	= 16	INTERM	<= 64	SUSC	> 32	RES	<= 1	SUSC	= 0.125	SUSC	
WHO 2011 S-11.5	*Salmonella* Havana	13,23:f,g:-	> 32	RES	> 4	RES	= 32	RES	> 256	RES	> 64	RES	= 0.03	SUSC	> 16	RES	<= 4	SUSC	> 128	RES	> 1024	RES	= 16	RES	> 32	RES	> 32	RES	ESBL-producer; *bla* (CTX-M15)
WHO 2011 S-11.6	*Salmonella* Onireke	3,10:d:1,7	> 32	RES	= 0.25	SUSC	= 0.38	SUSC	<= 0.25	SUSC	= 4	SUSC	= 1	RES	= 1	SUSC	= 16	SUSC	= 16	INTERM	<= 64	SUSC	<= 2	SUSC	<= 1	SUSC	= 0.125	SUSC	
WHO 2011 S-11.7	*Salmonella* Enteritidis	9,12:g,m:-	= 4	SUSC	= 0.5	SUSC	= 1	SUSC	= 0.25	SUSC	= 8	SUSC	= 0.06	SUSC	> 16	RES	<= 4	SUSC	= 128	RES	> 1024	RES	= 4	SUSC	<= 1	SUSC	= 0.064	SUSC	
WHO 2011 S-11.8	*Salmonella* Abaetetuba	11:k:1,5	<= 1	SUSC	<= 0.12	SUSC	= 0.25	SUSC	= 0.064	SUSC	= 8	SUSC	= 0.03	SUSC	= 1	SUSC	<= 4	SUSC	= 16	INTERM	<= 64	SUSC	<= 2	SUSC	<= 1	SUSC	= 0.064	SUSC	
WHO 2011 SH-11.1	*Shigella flexneri* type 6		= 4	SUSC	<= 0.125	SUSC	= 0.25	SUSC	= 0.032	SUSC	= 4	SUSC	<= 0.015	SUSC	= 1	SUSC	= 4	SUSC	= 16	SUSC	<= 64	SUSC	<= 2	SUSC	<= 1	SUSC	= 0.64	SUSC	
WHO 2011 SH-11.2	*Shigella sonnei*		> 32	RES	> 4	RES	= 4	RES	> 256	RES	= 4	SUSC	= 0.25	RES	= 2	SUSC	= 64	RES	> 128	RES	> 1024	RES	> 32	RES	> 32	RES	> 32	RES	ESBL-producer; *bla* (CMY-2)
WHO 2011 SH-11.3	*Shigella boydii* type 2		= 2	SUSC	<= 0.125	SUSC	= 0.25	SUSC	= 0.032	SUSC	<= 2	SUSC	= 0.25	RES	= 2	SUSC	= 64	RES	> 128	RES	> 1024	RES	<= 2	SUSC	> 32	RES	> 32	RES	
WHO 2011 SH-11.4	*Shigella flexneri* type 1b		> 32	RES	> 4	RES	= 4	RES	> 256	RES	> 64	RES	= 1	RES	= 2	SUSC	= 8	SUSC	> 128	RES	> 1024	RES	> 32	RES	> 32	RES	> 32	RES	ESBL-producer; bla(CTX-M15)

			Chloramphenicol		Ciprofloxacin		Erythromycin		Gentamicin		Nalidixic acid		Streptomycin		Tetracycline	
			CHL		**CIP**		**ERY**		**GEN**		**NAL**		**STR**		**TET**	
WHO 2011 C-11.1	*C. coli*		= 4	SUSC	> 4	RES	<= 0.5	SUSC	= 0.25	SUSC	= 64	RES	> 16	RES	<= 0.25	SUSC
WHO 2011 C-11.2	*C. coli*		= 4	SUSC	= 0.5	SUSC	> 32	RES	= 0.25	SUSC	= 8	SUSC	<= 1	SUSC	> 16	RES

WHO B-11.1	*Aeromonas hydrophila*

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WHO Collaborating Centre for Antimicrobial Resistance in Foodborne Pathogens
www.antimicrobialresistance.dk

PROTOCOL for

- serotyping and antimicrobial susceptibility testing of *Salmonella*
- serotyping and antimicrobial susceptibility testing of *Shigella*
- identification and antimicrobial susceptibility testing of *Campylobacter*
- identification of an unknown environmental bacterium

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1 INTRODUCTION

In 2000, the Global Foodborne Infections Network (formerly known as WHO Global Salm-Surv) launched an External Quality Assurance System (EQAS). The EQAS is organized by the National Food Institute, Technical University of Denmark (DTU Food), in collaboration with partners and Regional Sites in WHO GFN.

Various aspects of the proficiency test scheme may be subcontracted from time to time. When subcontracting occurs, it is placed with a competent subcontractor and the National Food Institute is responsible for the subcontractor's work.

The WHO EQAS 2011 includes:

- serotyping and antimicrobial susceptibility testing of eight *Salmonella* strains,
- serotyping and antimicrobial susceptibility testing of four *Shigella* strains,
- antimicrobial susceptibility testing of the *Escherichia coli* ATCC 25922 (CCM 3954), reference strain for quality control,
- identification and antimicrobial susceptibility testing of two thermophilic *Campylobacter* isolates,
- antimicrobial susceptibility testing of *Campylobacter jejuni* ATCC 33560 (CCM 6214), reference strain for quality control,

Technical University of Denmark
DTU

- identification of one 'unknown' bacterial isolate.

All participants will receive the strains according to the information they reported in the sign-up form.

The above mentioned reference strains are included in the parcel only for new participants of the EQAS who did not receive them previously. The reference strains are original CERTIFIED cultures provided free of charge, and should be used for future internal quality control for antimicrobial susceptibility testing in your laboratory. The reference strains will not be included in the years to come. Therefore, please take proper care of these strains. Handle and maintain them as suggested in the manual 'Subculture and Maintenance of QC Strains' available on the WHO CC website (please see www.antimicrobialresistance.dk).

2 OBJECTIVES

The main objective of this EQAS is to support laboratories to assess and, if necessary, improve the quality of serotyping and antimicrobial susceptibility testing of enteric human pathogens, especially *Salmonella*. A further objective is to assess and improve the comparability of surveillance data on *Salmonella* serotypes and antimicrobial susceptibility reported by different laboratories. Therefore, the laboratory work for this EQAS should be done by using the methods routinely used in your laboratory.

3 OUTLINE OF THE EQAS 2011

3.1 Shipping, receipt and storage of strains

In August/September 2011, some 180 laboratories located worldwide will receive a parcel containing eight *Salmonella* strains, four *Shigella* strains, two *Campylobacter* strains and one 'unknown' bacterial isolate (according to information reported in the sign-up form). An *E. coli* ATCC 25922 reference strain and a *C. jejuni* ATCC 33560 reference strain will be included for participants who signed up to perform antimicrobial susceptibility testing (AST) and did not receive them previously. All provided strains are non-toxin-producing human pathogens Class II. ESBL-producing strains could be included in the selected material.

Please confirm receipt of the parcel through the confirmation form enclosed in the shipment

The *Salmonella* and *Shigella* strains and the 'unknown' bacterial isolate are shipped as agar stab cultures, whereas the reference strains and the *Campylobacter* strains are shipped lyophilized. On arrival, the agar stab cultures must be subcultured and prepared for storage in your strain collection (e.g. in a -80 °C freezer). This set of cultures should serve as reference if discrepancies are detected during tests (e.g. they can be used if errors such as mis-labelling or contamination occur). Lyophilized strains must be reconstituted, and you can find below a suggested procedure.

3.2 Serotyping of *Salmonella*

The eight *Salmonella* strains should be serotyped by using the method routinely used in the laboratory. If you do not have all the necessary antisera, please go as far as you can in the identification and report the serogroup since also serogroup results will be evaluated. Serogroups should be reported by using terms according to Kauffmann-White-Le Minor (Grimont and Weill, 2007. 9th ed. Antigenic formulae of the *Salmonella* serovars. WHO Collaborating Centre for Reference and Research on *Salmonella*).

Please fill-in information concerning the brand of antisera used for typing in the fields available in the database for entering results. In addition, we kindly ask you to report which antisera you think is required to complete the serotyping, if relevant.

3.3 Antimicrobial susceptibility testing of *Salmonella*, *Shigella* and *E. coli* ATCC 25922

The *Salmonella* and *Shigella* strains and the *E. coli* ATCC 25922 reference strain should be tested for susceptibility towards as many as possible of the antimicrobials mentioned in the test form. Please use the methods routinely used in your laboratory.

For reconstitution of the *E. coli* reference strain, please see the document 'Instructions for opening and reviving lyophilized cultures' on the WHO CC website (please find the link at www.antimicrobialresistance.dk).

Testing of gentamicin and streptomycin susceptibility may be valuable for monitoring purposes. Therefore, we kindly ask you to disregard, for the purpose of this proficiency testing, that the Clinical and Laboratory Standards Institute (CLSI) guidelines state that *Salmonella* and *Shigella* should not be reported as susceptible to aminoglycosides.

The breakpoints used in this EQAS for interpreting MIC results are in accordance with CLSI values, and are supplemented with values from the European Committee on Antimicrobial Susceptibility Testing (EUCAST, www.eucast.org) and DTU Food (Table 1). Consequently, interpretation of MIC results will lead to categorization of strains into three categories: resistant (R), intermediate (I) and susceptible (S). In the evaluation report that you receive upon result submission, you can find that obtained interpretations in accordance with the expected interpretation will be defined as 'correct', whereas deviations from the expected interpretation will be defined as 'minor' (I ↔ S or I ↔ R), 'major' (S interpreted as R) or 'very major' (R interpreted as S).

Please report the breakpoints that you routinely use in your laboratory for interpretation of antimicrobial susceptibility test results in the fields available in the database (or in the test forms).

Concerning ciprofloxacin susceptibility test, please note that a low breakpoint has been used to determine the resistance category. This low breakpoint corresponds to the EUCAST

epidemiological cut-off value, which was established to take into consideration mechanisms of resistance like *qnr* genes or one point-mutation in the gyrase gene (Table 1; www.eucast.org). In this EQAS, microorganisms showing reduced susceptibility to ciprofloxacin are considered ciprofloxacin-resistant.

Table 1. Interpretive breakpoint for *Salmonella* and *Shigell*a antimicrobial susceptibility testing

Antimicrobials	Reference value, MIC (µg/mL)			Reference value, Disk diffusion (mm)		
	Sensitive	Intermediate	Resistant	Sensitive	Intermediate	Resistant
Ampicillin, AMP	≤8	16	≥32	≥17	14-16	≤13
Cefotaxime, CTX	≤1	-	>1	>27	-	≤27
Ceftazidime, CAZ	≤1	-	>1	>22	-	≤22
Ceftriaxone, CRO	≤1	-	>1	>25	-	≤25
Chloramphenicol, CHL	≤8	16	≥32	≥18	13-17	≤12
Ciprofloxacin, CIP	<0.125*	-	≥0.125*	≥23mm (1µg)*** or ≥30mm (5µg)***	-	<23mm (1µg)*** or <30mm (5µg)***
Gentamicin, GEN	≤4	8	≥16	≥15	13-14	≤12
Nalidixic acid, NAL	≤16	-	≥32	≥19	14-18	≤13
Streptomycin, STR	≤8**	16**	≥32**	≥15	12-14	≤11
Sulfonamides, SMX	≤256	-	≥512	≥17	13-16	≤12
Tetracycline, TET	≤4	8	≥16	≥15	12-14	≤11
Trimethoprim, TMP	≤8	-	≥16	≥16	11-15	≤10
Trimethoprim + sulfamethoxazole, TMP+SMX, SXT	≤2/38	-	≥4/76	≥16	11-15	≤10

Reference values used in this EQAS are according to CLSI, with the following exceptions:
* EUCAST (epidemiological cut-off values)
** DTU Food
*** In the absence of values provided by EUCAST, the article by Cavaco LM and Aarestrup FM (J. Clin. Microbiol. 2009. Sep;47(9):2751-8) provides the background for these interpretative criteria in the WHO GFN EQAS. In that article, *Shigella* was not included. However, the same interpretative criteria will be used in this context.

Important notes*: beta-lactam resistance*

The following tests for detection of Extended-Spectrum Beta-Lactamase (ESBL) production are optional:

All strains showing reduced susceptibility to cefotaxime (CTX), ceftazidime (CAZ) and/or ceftriaxone (CRO) could be tested for ESBL production by confirmatory test.
Confirmatory test for ESBL production requires use of both cefotaxime (CTX) and ceftazidime (CAZ) alone and in combination with a β-lactamase inhibitor (clavulanic acid). Synergy is defined either as i) a ≥ 3 twofold concentration decrease in an MIC for either antimicrobial agent tested in combination with clavulanic acid vs. its MIC when tested alone (E-test 3 dilution steps difference; MIC CTX : CTX/CL or CAZ : CAZ/CL ratio ≥ 8) or ii) a ≥ 5 mm increase in a zone diameter for either antimicrobial agent tested in combination with clavulanic acid vs. its zone when tested alone (CLSI M100 Table 2A; Enterobacteriaceae). The presence of synergy indicates ESBL production.

Of note, MIC values and relative interpretation of cefotaxime (CTX), ceftazidime (CAZ) and/or ceftriaxone (CRO) used for detection of beta-lactamase-producing strains in this EQAS should be reported as found, which is in accordance with EUCAST expert rules.

3.4 Handling the *Campylobacter* strains

Freeze-dried cultures are supplied in vacuum-sealed ampoules. Care should be taken in opening the ampoule, and all instructions given below should be followed closely to ensure the safety of the person who opens the ampoule and to prevent contamination of the culture.

a. Check the number of the culture written on the label.
b. Make a file cut on the ampoule just above the shoulder of the ampoule.
c. Disinfect the ampoule with alcohol-dampened gauze or alcohol-dampened cotton wool.
d. Crack the glass using sterile gauze or cotton to protect your fingers.
e. Add to the dried suspension about 0.5 ml of appropriate broth or sterile 0.9% NaCl solution by using a pipette. Mix carefully to avoid creating aerosols.
f. Inoculate the suspension on a suitable agar plate with a 10 µl loop or a cotton swab.
g. Transfer the rest of the content of the ampoule to a test tube containing 5-6 ml of a suitable liquid media.
h. Incubate the agar plate and liquid media at a temperature of 42°C at microaerobic conditions for 24-48 hours.
i. Inoculate a second agar plate from the liquid media with a 10 µl loop or a cotton swab if the initial plate had inadequate growth.
j. Select a pure culture with vigorous growth from the agar plate for further work.

Please note that:

- Cultures may need at least one subculture before they can be optimally used

- Unopened ampoules should be kept in a dark and cool place!

For reconstitution of *C. jejuni* ATCC 33560 reference strain: please see the document 'Instructions for opening and reviving lyophilised cultures' on the WHO CC website (please find the link at www.antimicrobialresistance.dk).

3.5 Identification of *Campylobacter*

The two thermophilic *Campylobacter* isolates should be identified to the species level.

3.6 Antimicrobial susceptibility testing of *Campylobacter* and *C. jejuni* ATCC 33560

The *Campylobacter* test strains and the *C. jejuni* reference strain should be tested for susceptibility to as many antimicrobials as possible among the ones mentioned in the test form. Please note that only MIC methods (i.e. broth or agar dilution methods) are recommendable for AST of *Campylobacter*. Neither the use of disk diffusion nor E-test is recommendable for AST of *Campylobacter*.

In this EQAS, the breakpoints used for interpretation of MIC results for *Campylobacter* are epidemiological cut-off values according to EUCAST (www.eucast.org; Table 2). Consequently, only two categories of characterization (resistant, R and sensitive, S) are allowed. In the evaluation report that you receive upon result submission, you can find that obtained interpretations that are in agreement with the expected interpretation will be categorized as 'correct', whereas deviations from the expected interpretation will be categorized as 'incorrect'.

Please report the breakpoints that you routinely use in your laboratory for interpretation of antimicrobial susceptibility test results in the fields available in the database (or in the test forms).

Please note that the interpretation of antimicrobial susceptibility test results for *Campylobacter* requires knowledge of the *Campylobacter* species. If you did not sign up for *Campylobacter* identification but you perform AST on *Campylobacter*, you are welcome to contact the EQAS Coordinator to obtain information regarding the identity of the *Campylobacter* test strains.

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Table 2. Interpretive criteria for *Campylobacter* antimicrobial susceptibility testing

Antimicrobials for *Campylobacter*	*C. jejuni*	*C. coli*
	MIC (µg/mL) **R is >**	MIC (µg/mL) **R is >**
Chloramphenicol, CHL	16	16
Ciprofloxacin, CIP	1	1
Erythromycin, ERY	4	16
Gentamicin, GEN	1	2
Nalicixic acid, NAL	16	32
Streptomycin, STR	2	4
Tetracycline, TET	2	2

Reference values for interpretation of Campylobacter *AST results according to EUCAST*

The sub-cultured *Campylobacter* strains should be used for MIC testing after incubation at 36-37ºC for 48 hours or at 42ºC for 24 hours. Likely, two subcultures are needed prior to MIC testing to ensure optimal growth.

3.7 Identification of the unknown environmental bacterium

The 'unknown' isolate should be identified to the species level and further typed if relevant.

4 REPORTING OF RESULTS AND EVALUATION

Please write your results in the enclosed test forms, and enter your results into the interactive web database.
We recommend reading carefully the description reported in paragraph 5 before entering your results in the web database. For entering your results via the web, you will be guided through all steps on the screen and you will immediately be able to view and print a report evaluating your results. Results in agreement with the expected interpretation are categorized as 'correct', while results deviating from the expected interpretation are categorized as 'incorrect'.

Results must be submitted no later than 31 December 2011.

If you do not have access to the Internet, or if you experience difficulties in entering your results, please return the completed test forms by e-mail, fax or mail to the National Food Institute, Denmark.

All results will be summarized in a report available to all participants. Individual results will be anonymous and will only be forwarded to the official GFN Regional Centre in your region.

We are looking forward to receiving your results!

If you have any questions or concerns, please do not hesitate to contact the EQAS Coordinator:

Susanne Karlsmose
National Food Institute, Technical University of Denmark
Kemitorvet, Building 204 ground floor, DK-2800 Lyngby - DENMARK
Tel: +45 3588 6601, Fax: +45 3588 6341
E-mail: suska@food.dtu.dk

Please note that it is also possible to communicate with the EQAS organizers in languages different from English. However, this is not a direct contact with the EQAS organizers since translation of the message is required. The following languages may be used: Chinese, French, Portuguese, Russian and Spanish.

5 HOW TO ENTER RESULTS IN THE INTERACTIVE DATABASE

Please read these instruictions before entering the web page. Remember that you need by your side the completed test forms and the breakpoint values you used.

In general, you navigate in the database with the Tab-key and mouse and, at any time, a click on the WHO logo takes you back to the main menu.

1) Enter the WHO CC website (link available at http://www.antimicrobialresistance.dk), then
    a. Click on ‘EQAS’
    b. Click on the link for the interactive database
    c. Write your username and password in lower-case letters and click on ‘Login’.
    You can find your username and password in the letter accompanying your parcel.
    Your username and password will remain unchanged in future trials.

2) Click on ‘Materials and methods’
    a. Fill-in the fields relative to brand of antisera (very important because we would like to compare results obtained with different brands of antisera)
    b. Fill-in the fields relative to the method used for antimicrobial susceptibility testing
    c. Enter the brand of materials, e.g. Oxoid
    d. Fill-in the field asking whether your institute serves as a national reference laboratory
    e. In the comment field, report which antisera you think is required to complete your serotyping, if relevant
    f. Click on ‘Save and go to next page’ – REMEMBER TO SAVE EACH PAGE BEFORE LEAVING IT!

3) In the data entry page ‘Routinely used breakpoints’

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a. Fill-in the fields relative to the breakpoints used routinely in your laboratory to determine the antimicrobial susceptibility category. Remember to use the operator keys in order to show: equal to (=), less than (<), less or equal to (≤), greater than (>) or greater than or equal to (≥).

b. In the data entry pages '*Salmonella* strains 1-8'
c. SELECT the serogroup (O-group) from the drop-down list, DO NOT WRITE – Wait a few seconds – the page will automatically reload, so that the drop-down list in the field "Serotype" only contains serotypes belonging to the chosen serogroup.
d. SELECT the serotype from the drop-down list – DO NOT WRITE – wait a few seconds and you can enter the antigenic formula (e.g. 1,4,5,12:i:1,2)
e. Enter the zone diameters in mm or MIC values in µg/ml. Remember to use the operator keys to show e.g. equal to (=), etc…
f. Enter the interpretation as R (resistant), I (intermediate) or S (susceptible)
g. If you performed confirmatory tests for ESBL production, please choose the appropriate result from the pick list.
h. If relevant, fill-in the field related to comments (e.g. which antisera you miss for complete serotyping, etc…)
i. Click on 'Save and go to next page'

If you did not perform these tests, please leave the fields empty

4) In the data entry page '*E. coli* reference strain':
   a. Enter the zone diameters in mm or MIC values in µg/ml. Remember to use the operator keys to show e.g. equal to (=), etc…
   b. Click on 'Save and go to next page'

5) In the page 'Identification of *Campylobacter* and unknown sample':
   a. Choose the correct *Campylobacter* species from the pick list
   b. Fill-in the field concerning species and type of the unknown bacterial isolate, and report the method used for identification
   c. Click on 'Save and go to next page'

   If you did not perform these tests, please leave the fields empty

6) The next page is a menu that allows you to review the input pages and approve your input *and finally see and print the evaluated results*
   a. Browse through the input pages and make corrections if necessary. Remember to click on 'save and go to next page' if you make any corrections.

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b. Approve your input. Be sure that you have filled-in all the results before approval, as YOU CAN ONLY APPROVE ONCE! The approval blocks your data entry into the interactive database, but allows you to see the evaluated results.
c. As soon as you have approved your input, an evaluation report will appear.

7) After browsing all pages in the report, you will find a new menu. You can choose 'EQAS 2011 start page', 'Review evaluated results' (a printer friendly version of the evaluation report is also available) or 'Go to Global Salm-Surv homepage'.

End of entering your data – thank you very much!

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SUBCULTURE AND MAINTENANCE OF QUALITY CONTROL STRAINS

1.1 Purpose

Improper storage and repeated subculturing of bacteria can produce alterations in antimicrobial susceptibility test results. The Clinical and Laboratory Standards Institute (CLSI, formerly NCCLS) has published a guideline for Quality Control (QC) stock culture maintenance to ensure consistent antimicrobial susceptibility test results.

1.2 References

M100-S21, January 2011 (Performance Standards for Antimicrobial Susceptibility Testing)

M7-A8, January 2009 (Methods for Dilution Antimicrobial Susceptibility Test for Bacteria That Grow Aerobically; Approved Standard)

1.3 Definition of Terms

Reference Culture: A reference culture is a microorganism preparation that is acquired from a culture type collection.

Reference Stock Culture: A reference stock culture is a microorganism preparation that is derived from a reference culture. Guidelines and standards outline how reference stock cultures must be processed and stored.

Working Stock Cultures: A working stock culture is growth derived from a reference stock culture. Guidelines and standards outline how working stock cultures must be processed and how often they can be subcultured.

Subcultures (Passages): A subculture is simply the transfer of established microorganism growth on media to fresh media. The subsequent growth on the fresh media constitutes a subculture or passage. Growing a reference culture or reference stock culture from its preserved status (frozen or lyophilized) is not a subculture. The preserved microorganism is not in a stage of established growth until it is thawed or hydrated and grown for the first time

1.4 Important Considerations

- Do not use disc diffusion strains for MIC determination.
- Obtain QC strains from a reliable source such as ATCC
- CLSI requires that QC be performed either on the same day or weekly (only after 30 day QC validation)
- Any changes in materials or procedure must be validated with QC before implemented
- For example: Agar and broth methods may give different QC ranges for drugs such as glycopeptides, aminoglycosides and macrolides

- Periodically perform colony counts to check the inoculum preparation procedure
- Ideally, test values should be in the middle of the acceptable range
- Graphing QC data points over time can help identify changes in data helpful for troubleshooting problems

1.5 Storage of Reference Strains

Preparation of stock cultures

- Use a suitable stabilizer such as 50% fetal calf serum in broth, 10-15% glycerol in tryptic soy broth, defibrinated sheep blood or skim milk to prepare multiple aliquots.
- Store at -20°C, -70°C or liquid nitrogen. (Alternatively, freeze dry.)
- Before using rejuvenated strains for QC, subculture to check for purity and viability.

Working cultures

- Set up on agar slants with appropriate medium, store at 4-8°C and subculture weekly.
- Replace the working strain with a stock culture at least monthly.
- If a change in the organisms inherent susceptibility occurs, obtain a fresh stock culture or a new strain from a reference culture collection e.g. ATCC.

1.6 Frequency of Testing

Weekly vs. daily testing

Weekly testing is possible if the lab can demonstrate satisfactory performance with daily testing as follows:

- Documentation showing reference strain results from 30 consecutive test days were within the acceptable range.
- For each antimicrobial/organism combination, no more than 3 out of 30 MIC values may be outside the acceptable range.

When the above are fulfilled, each quality control strain may be tested once a week and whenever any reagent component is changed.

Corrective Actions

If an MIC is outside the range in weekly testing, corrective action is required as follows:

- Repeat the test if there is an obvious error e.g. wrong strain or incubation conditions used
- If there is no obvious error, return to daily control testing

The problem is considered resolved only after the reference strain is tested for 5 consecutive days and each drug/organism result is within specification on each day.

If the problem cannot be resolved, continue daily testing until the errors are identified.

Repeat the 30 days validation before resuming weekly testing.

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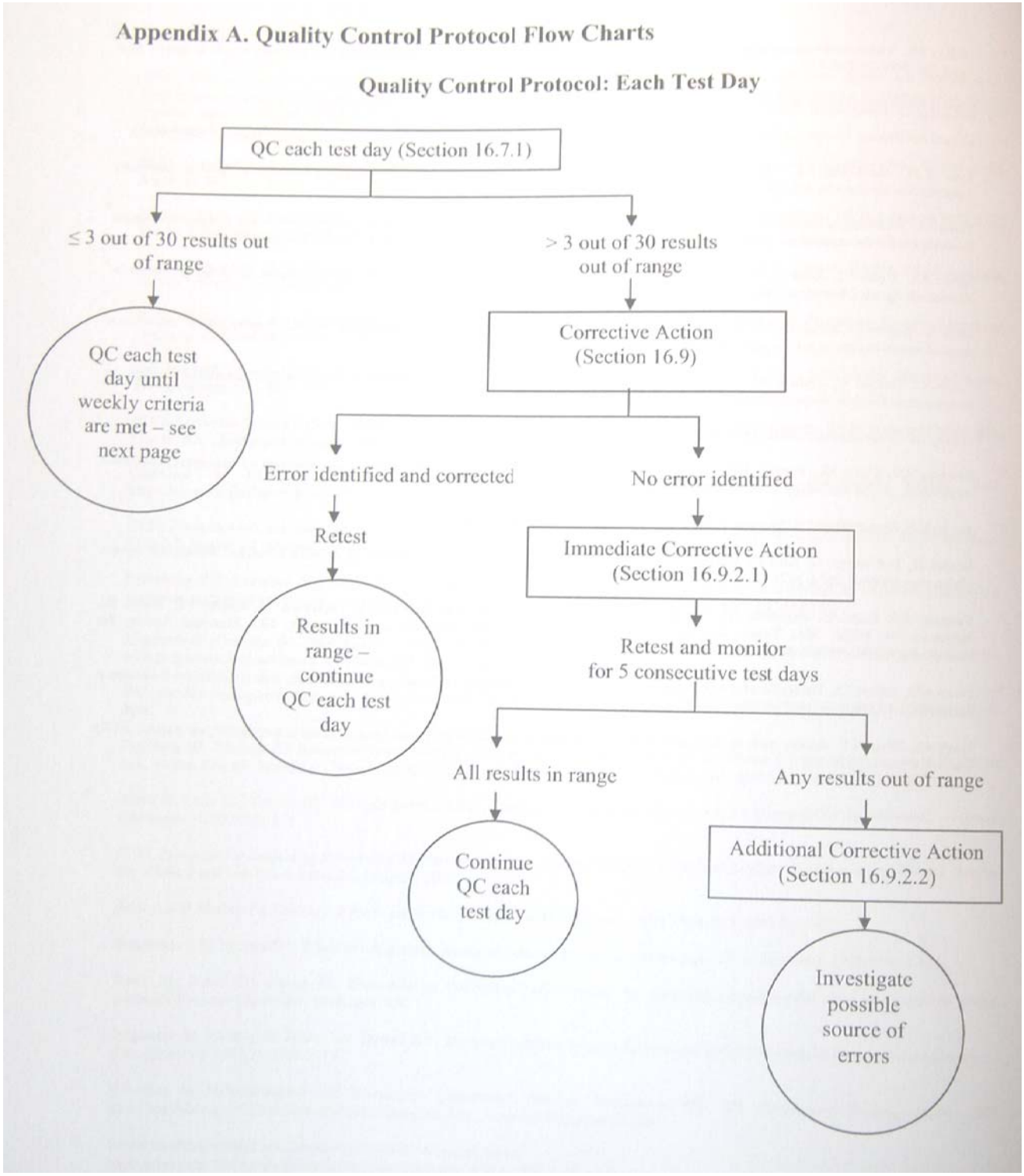
DAILY MIC QC CHART



Reference: CLSI M7-A8, page 44

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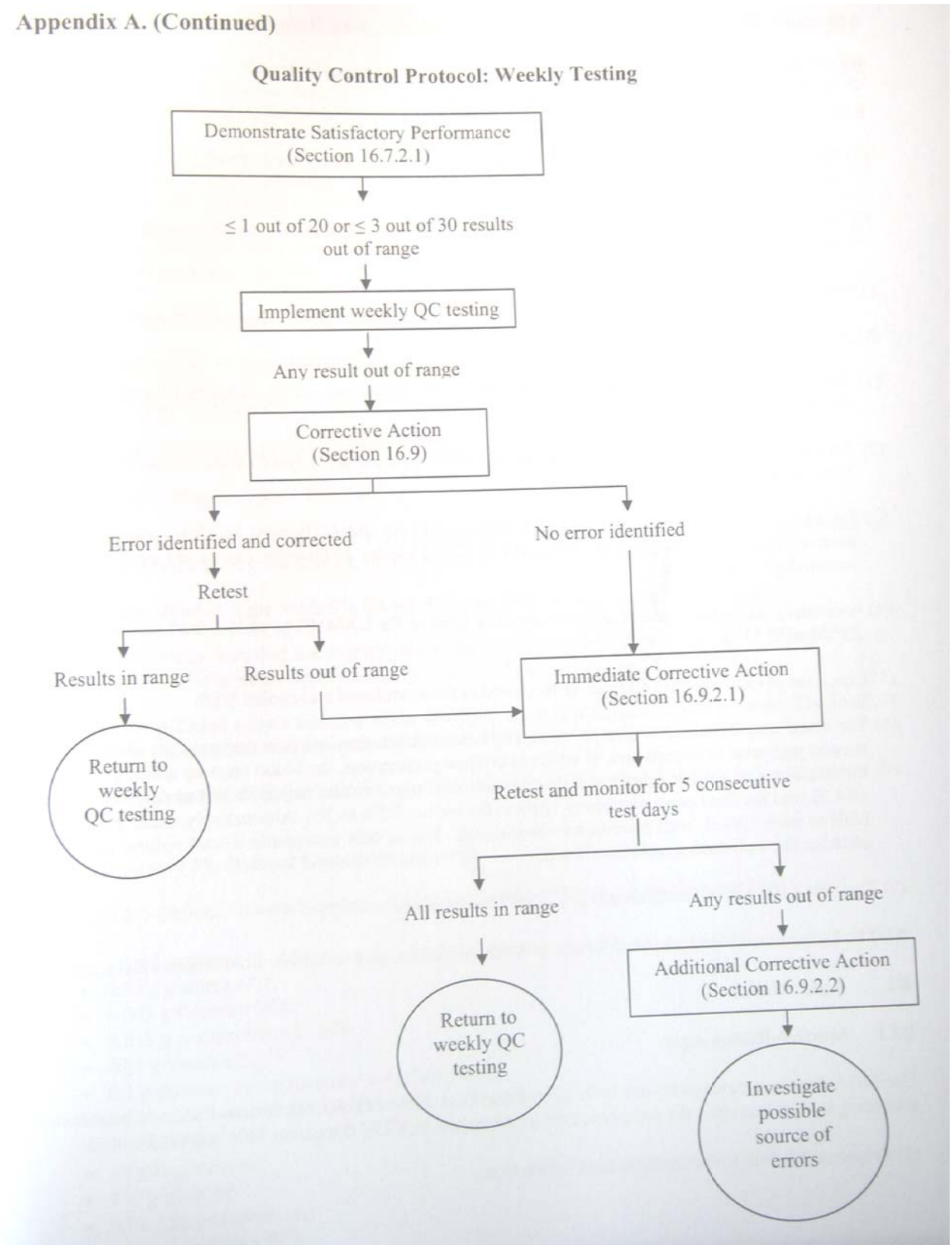
WEEKLY MIC QC CHART

Appendix A. (Continued)



Reference: CLSI M7-A8, page 45

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INSTRUCTIONS FOR OPENING AND REVIVING LYOPHILISED CULTURES

Manual from Czech Collection of Microorganisms (CCM)
Masaryk University
Tvrdého 14
602 00 BRNO
Czech Republic

Lyophilised cultures are supplied in vacuum-sealed ampoules. Care should be taken in opening the ampoule. All instructions given below should be followed closely to ensure the safety of the person who opens the ampoule and to prevent contamination of the culture.

a. Check the number of the culture on the label inside the ampoule
b. Make a file cut on the ampoule near the middle of the plug
c. Disinfect the ampoule with alcohol-dampened gauze or alcohol-dampened cotton wool from just below the plug to the pointed end
d. Apply a red-hot glass rod to the file cut to crack the glass and allow air to enter slowly into the ampoule
e. Remove the pointed end of the ampoule into disinfectant
f. Add about 0.3 ml appropriate broth to the dried suspension using a sterile Pasteur pipette and mix carefully to avoid creating aerosols. Transfer the contents to one or more suitable solid and /or liquid media
g. Incubate the inoculated medium at appropriate conditions for several days
h. Autoclave or disinfect effectively the used Pasteur pipette, the plug and all the remains of the original ampoule before discarding

Please note that:

- Cultures should be grown on media and under conditions as recommended in the CCM catalogue
- Cultures may need at least one subculturing before they can be optimally used in experiments
- Unopened ampoules should be kept in a dark and cool place!

National Food Institute
Technical University of Denmark
Mørkhøj Bygade 19
DK - 2860 Søborg

Tel. 35 88 70 00
Fax 35 88 70 01

www.food.dtu.dk

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